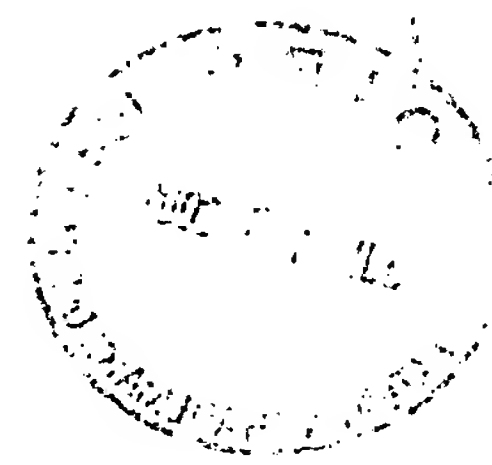


	MS-GPC- 8-27-7	MS-GPC- 8-27-10	MS-GPC- 8-6-13	MS-GPC- 8-27-41	MS-GPC- 8-6-47	MS-GPC- 8-10-57	MS-GPC- 8-6-27	MS-GPC- 8	MS-GPC- 8-6
Plastic	-0.004	-0.020	-0.022	-0.025	-0.001	0.005	0.007	-0.022	-0.018
BSA	-0.003	-0.019	-0.021	-0.022	0.008	0.003	0.003	-0.016	-0.019
Testosterone									
-BSA	-0.005	-0.010	-0.012	-0.007	0.011	0.003	0.002	-0.009	-0.012
Lysozyme	-0.005	-0.079	-0.079	-0.073	0.013	0.014	0.006	-0.081	-0.072
human									
Apotransferrin	-0.009	-0.016	-0.018	-0.018	-0.005	-0.008	-0.004	-0.014	-0.016
MHCII (DRA*0101/ DRB1*0401)	1.549	1.493	1.467	1.525	1.400	1.256	1.297	1.058	1.306

Fig. 1A



#5

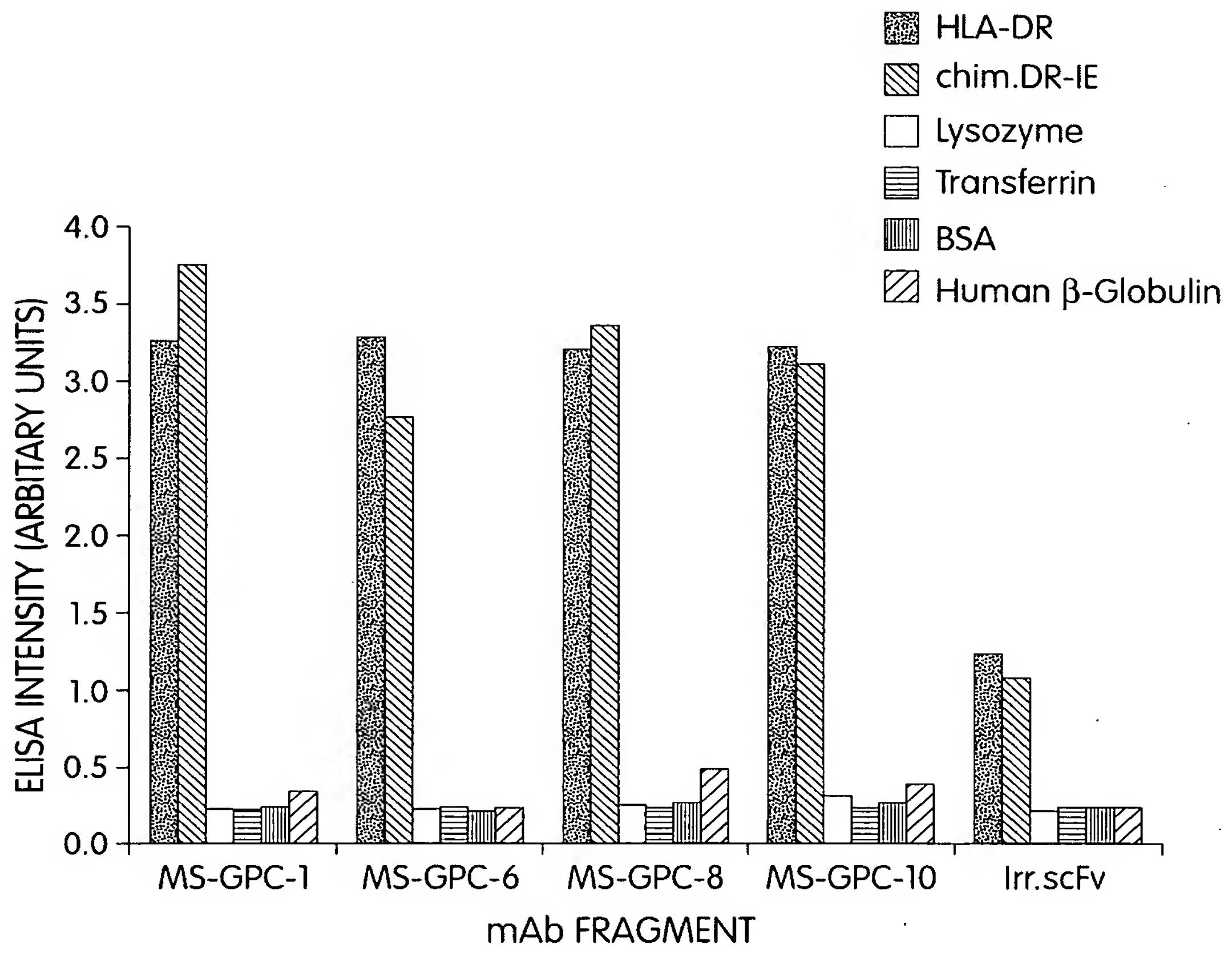


Fig. 1B

Target Proteins	scFv												IgG		
	17	2E	45	5C	73	8A	A1	B8	E6	FD	159	170	1D09C3	1C7277	305D3
DR4Dw4 Purified	+ <sup>a</sup>	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Chimeric DR-IE purified	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Lysozyme	- <sub>b</sub>	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Transferrin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BSA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Human gamma globulin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

a. In Elisa, OD (at 370 nm - background): > 1.5  
b. In Elisa, OD (at 370 nm - background): < 0.5

Fig. 1C

Cell Line	HLA-	DRB1*	scFv													IgG			
			17	2E	45	5C	73	8A	A1	B8	E6	FD	159	170	1D09C3	1C7277	305D3		
LG2	DR1	0101	+ <sup>a</sup>	+	- <sup>b</sup>	-	+	+	+	+	+	+	+	+	+	+	+		
E4181324	DR2	15021	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+		
VAVY	DR3	0301	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+		
PRIESS	DR4Dw4	0401	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+/- <sup>c</sup>		
TS10	DR4Dw10	0402	+	+	-	+/-	+	+	+	+	+	+	+	+	+	+	+		
BIN40	DR4Dw14	0404	+	+	+	+/-	+	+	+	+	+	+	+	+	+	+	+		
TAB089	DR8	8031	+	+	-	+/-	+	+	+	+	+	+	+	+	+	+	+		
DKB	DR9	9012	+	+	+/-	+/-	+	+	+	+	+	+	+	+	+	+	+/-		
WT47	DR13	1302	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+		
TEM	DR14	1401	+	+	+	+/-	+	+	+	+	+	+	+	+	+	+	+		
L105.1	DRw52	B3*0101	+	-	-	-	nt <sup>d</sup>	+	-	+	+	+	nt	nt	+/-	+/-	+/-		
L257.6	DRw53	B4*0101	+/-	-	+	-	nt	+	-	+	+/-	+/-	nt	nt	+	+	+		
L25.4	DPw4/w4.2	DP0103/0402	-	-	-	-	nt	+	-	-	-	-	nt	nt	+/-	-	+/-		
L256.12	DPw2/w2.1	DP0202/0201	-	-	-	-	nt	+/-	-	-	-	-	nt	nt	-	-	-		
L21.3	DQ7/w2	DQ0201/0602	-	-	-	-	nt	+	-	+	-	-	nt	nt	nt	nt	nt		
Target Cell			% Cells Killed <sup>e</sup>																
PRIESS			75	20	28	32	22	89	33	59	75	34	1	5	88	93	74		

a. FACS analysis, mAb + FITC-anti human IgG<sub>4</sub>, mean fluorescence intensity > 30.

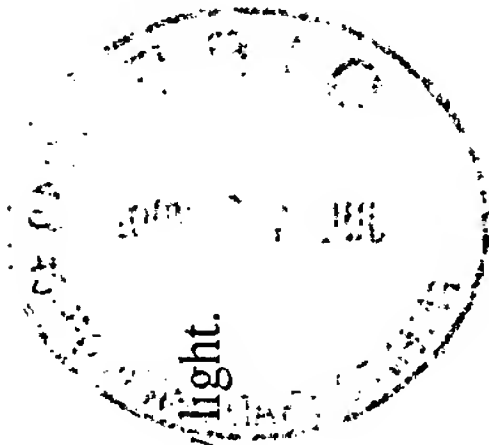
b. Mean fluorescence intensity < 10.

c. Mean fluorescence intensity 10-30.

d. Not tested.

e. Based on viable cell recovery after treatment with 200nM scFv plus 100 nM anti-FLAG or 50 nM mab at 37°C for 4h. Determined by light.

Fig. 2



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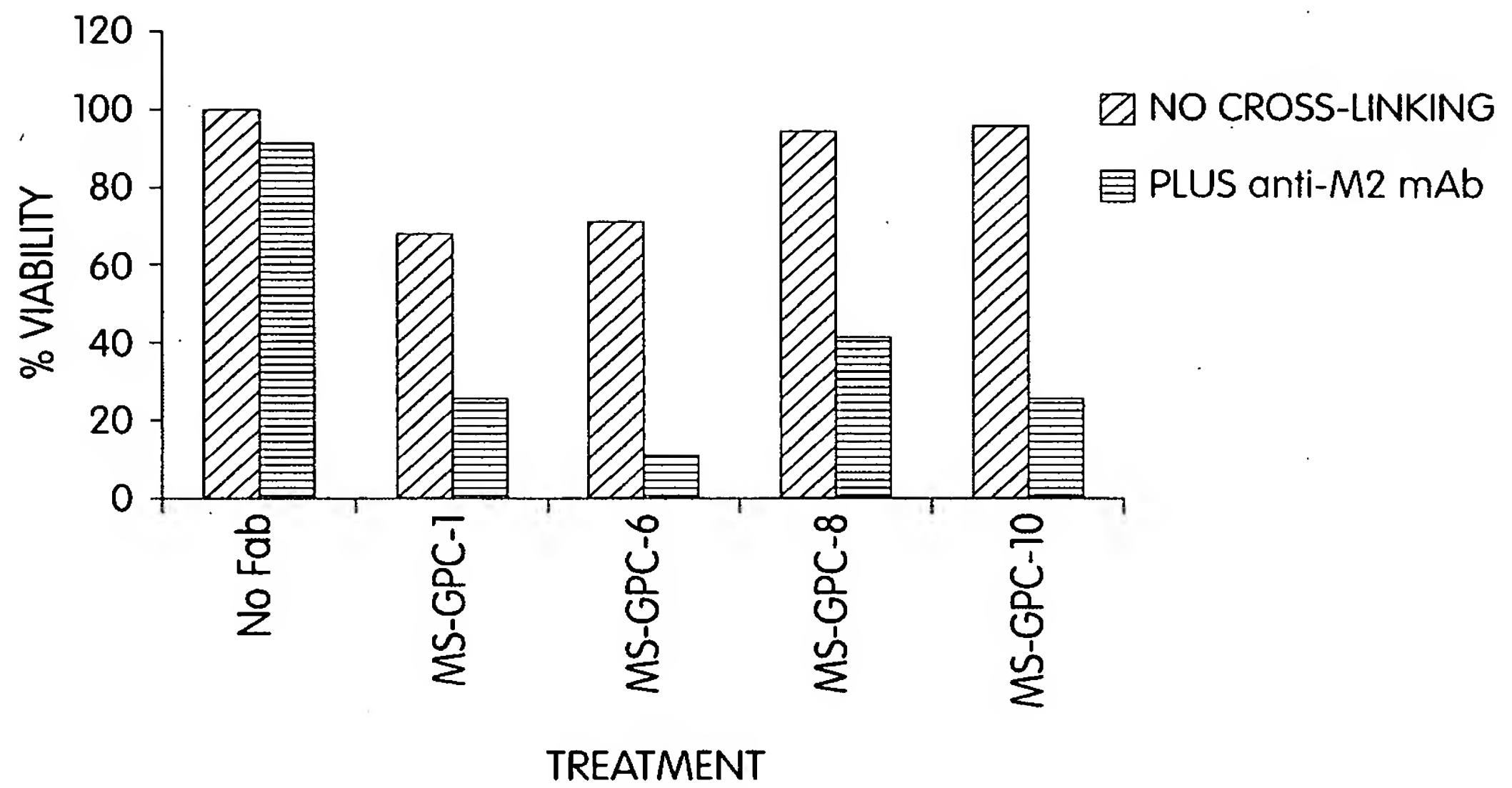


Fig. 3

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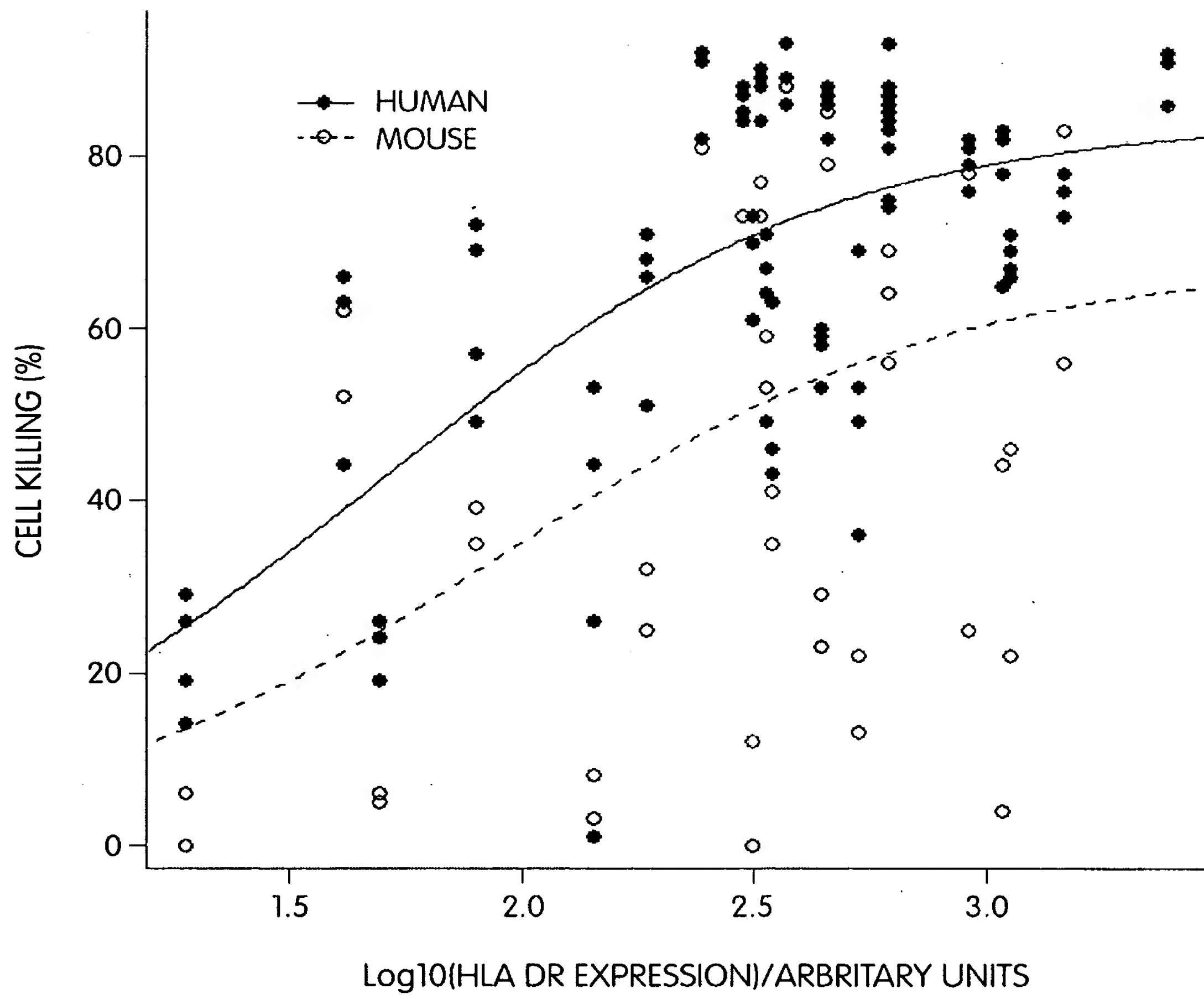
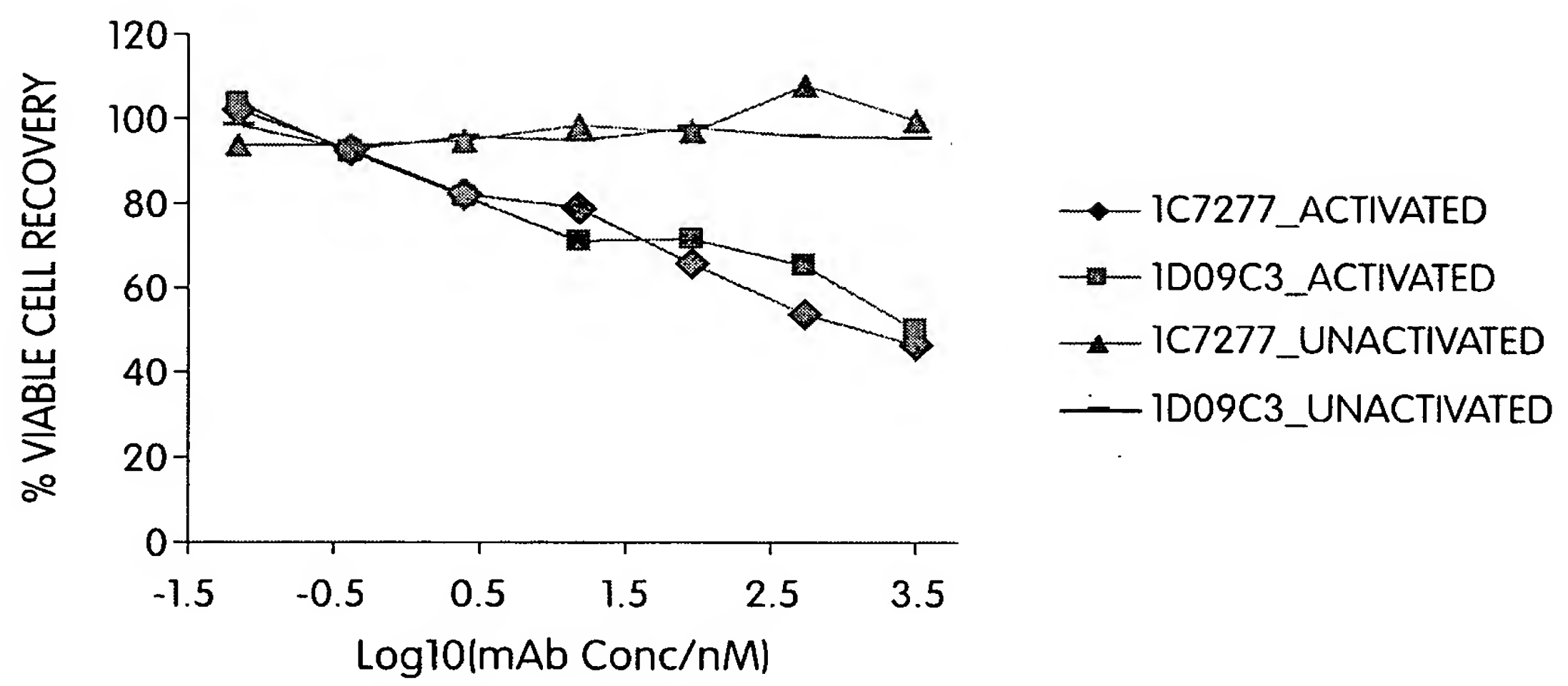


Fig. 4



**Fig. 5**

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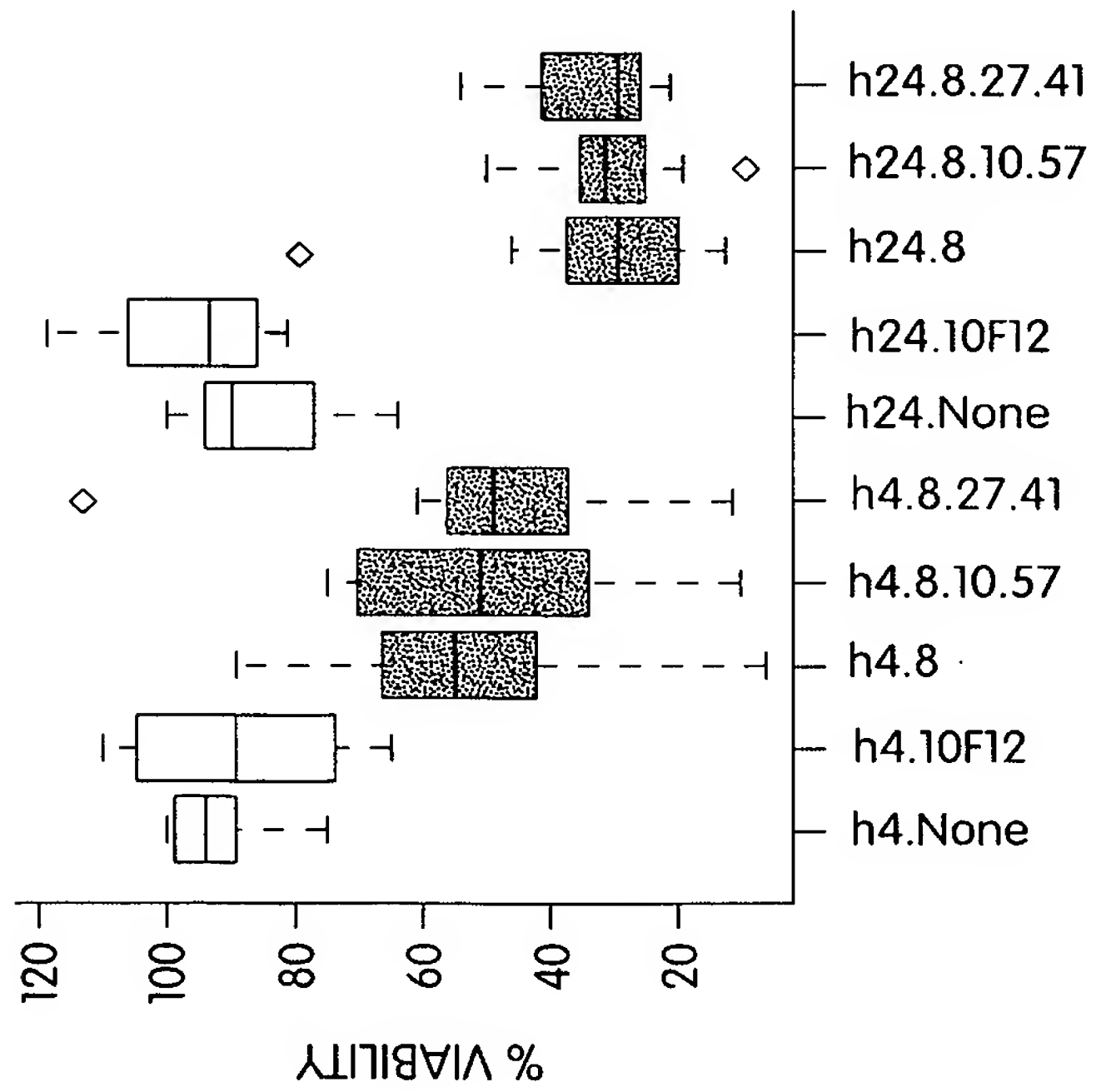
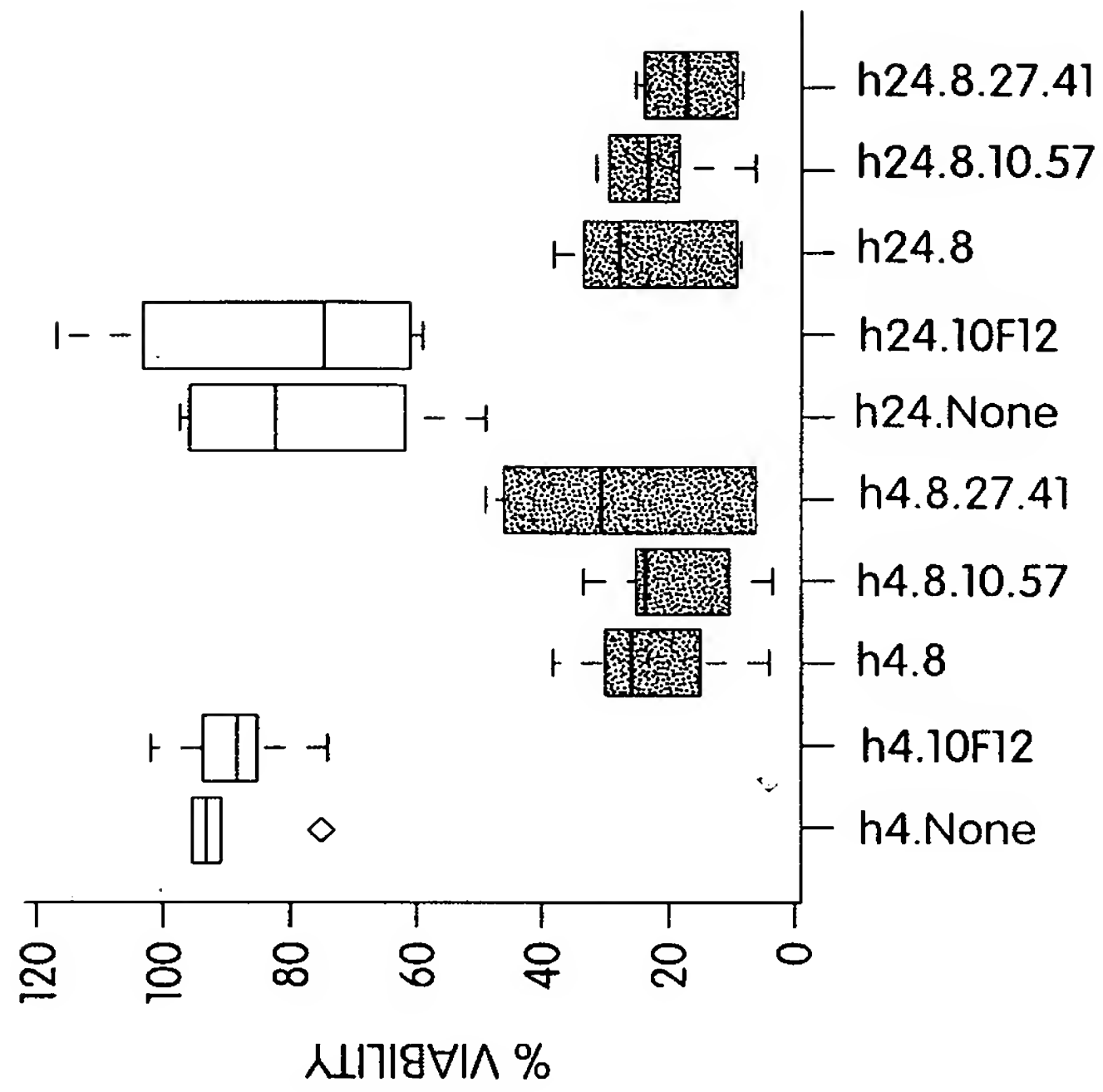


Fig. 6A



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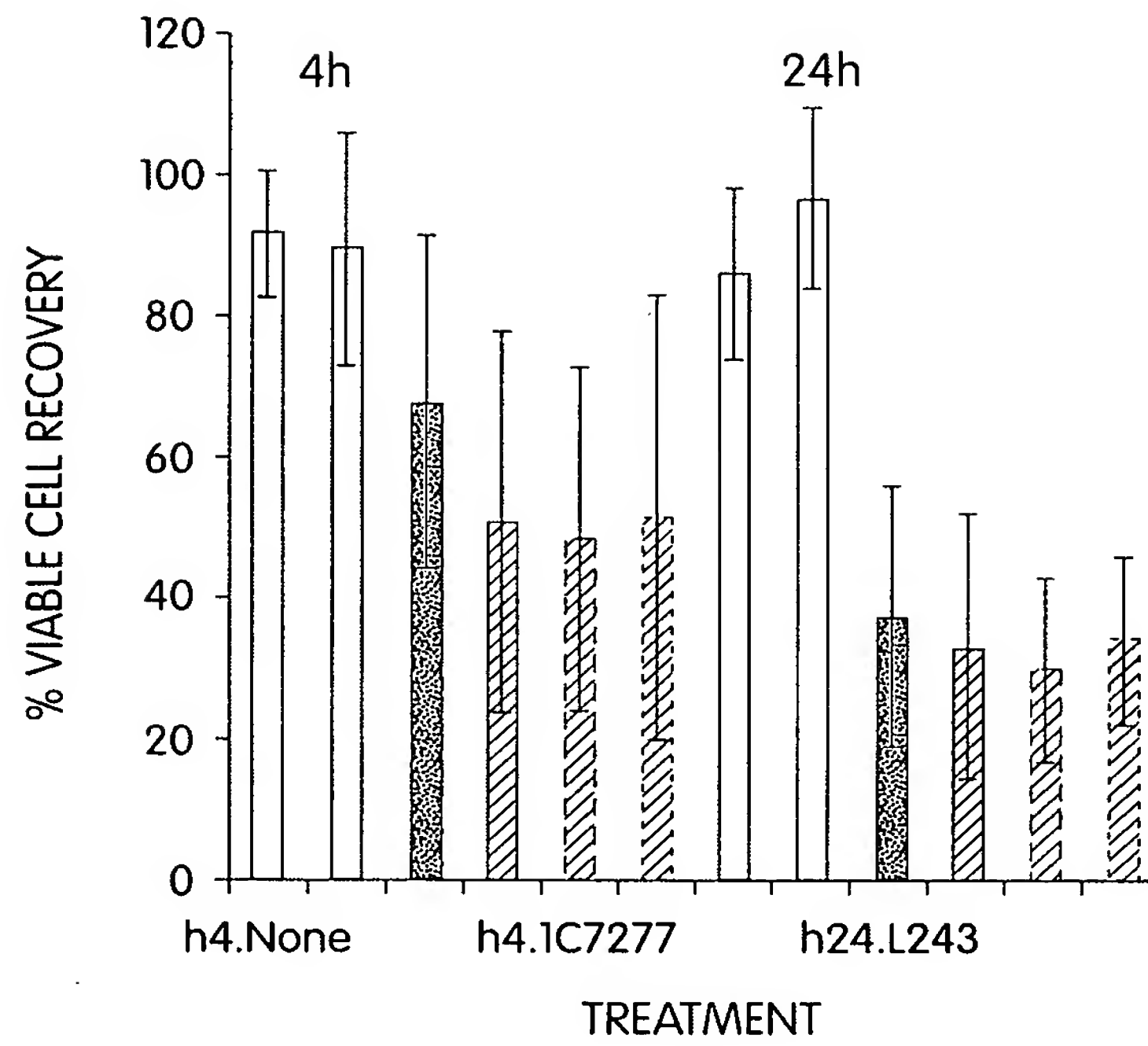


Fig. 6B

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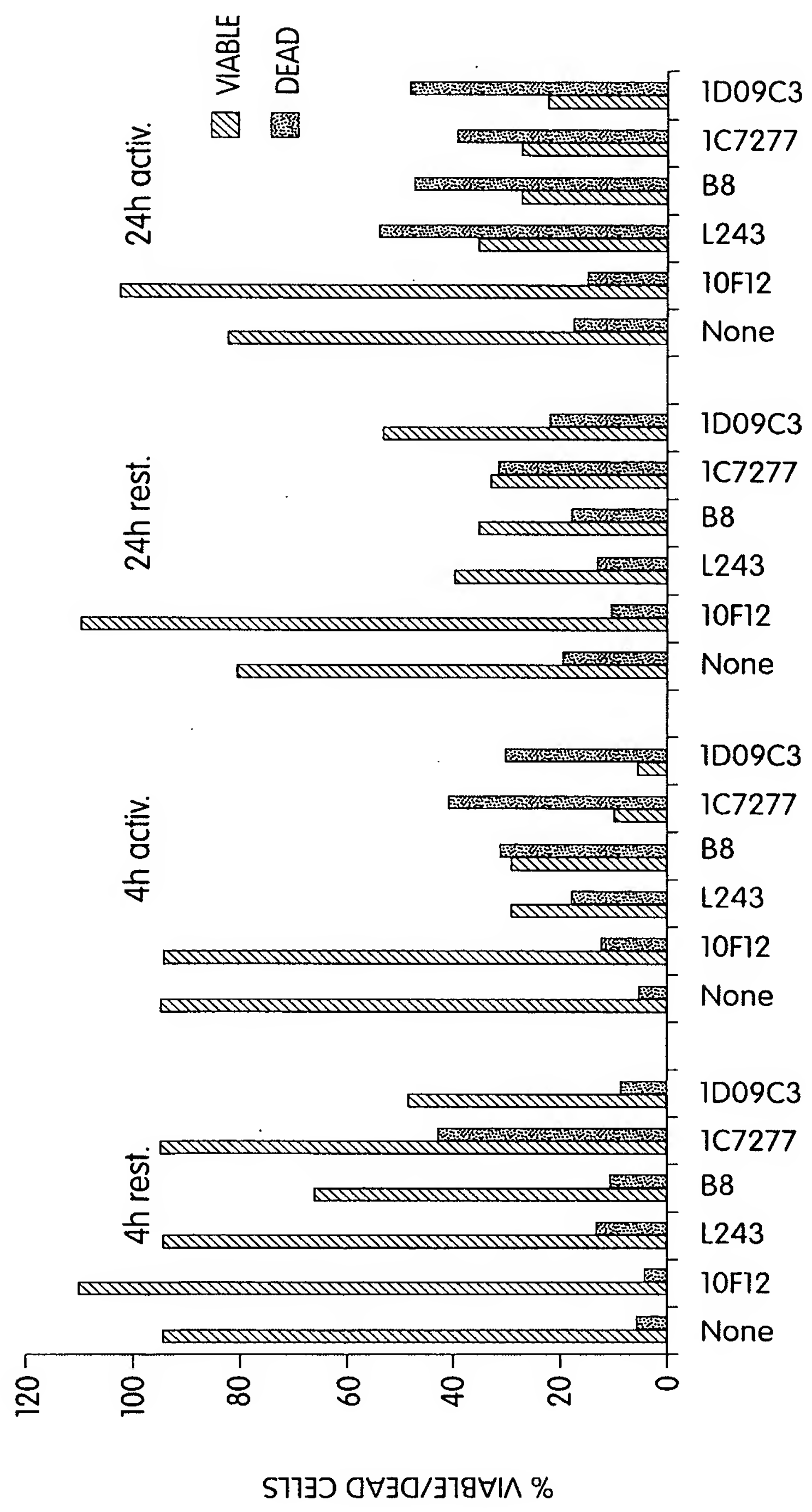
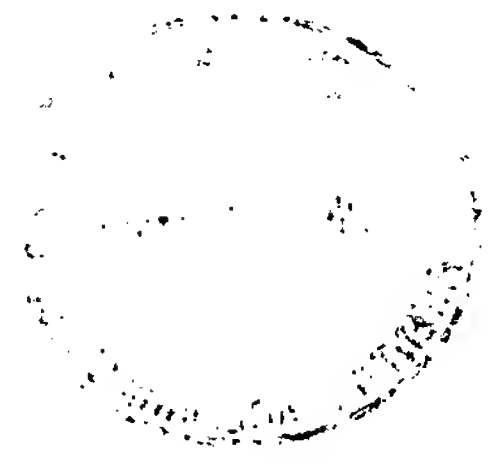


Fig. 6C

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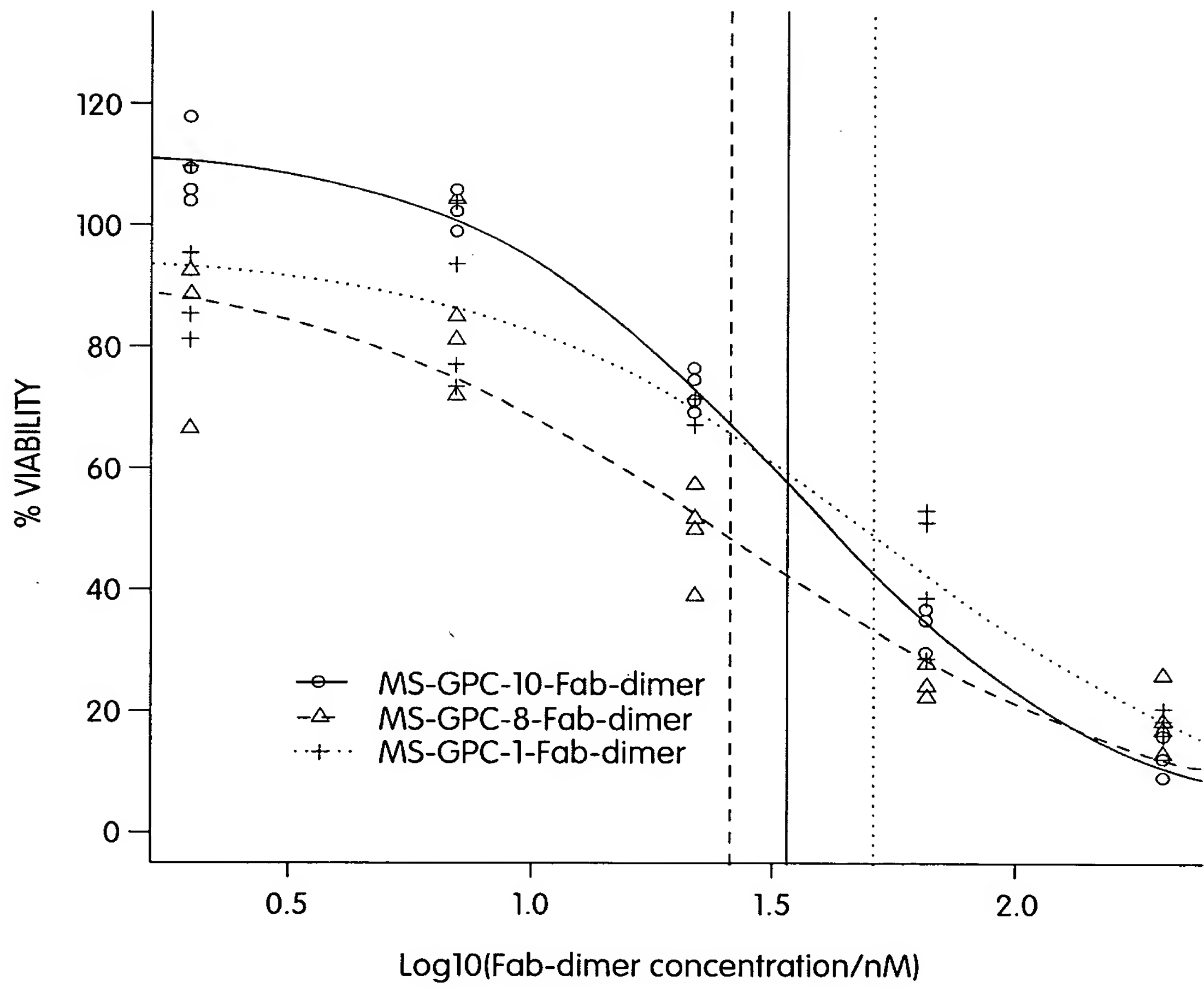


Fig. 7A

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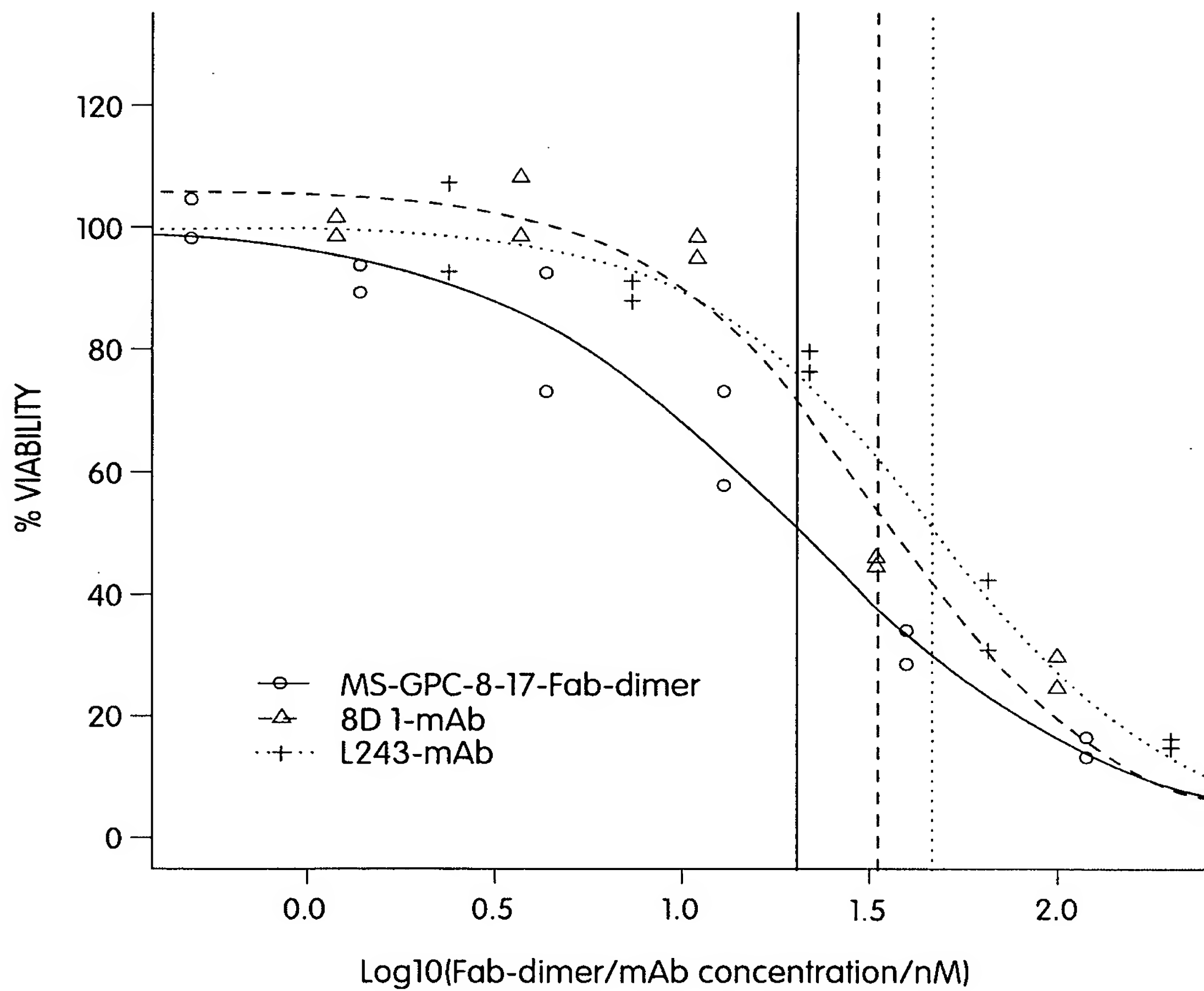


Fig. 7B

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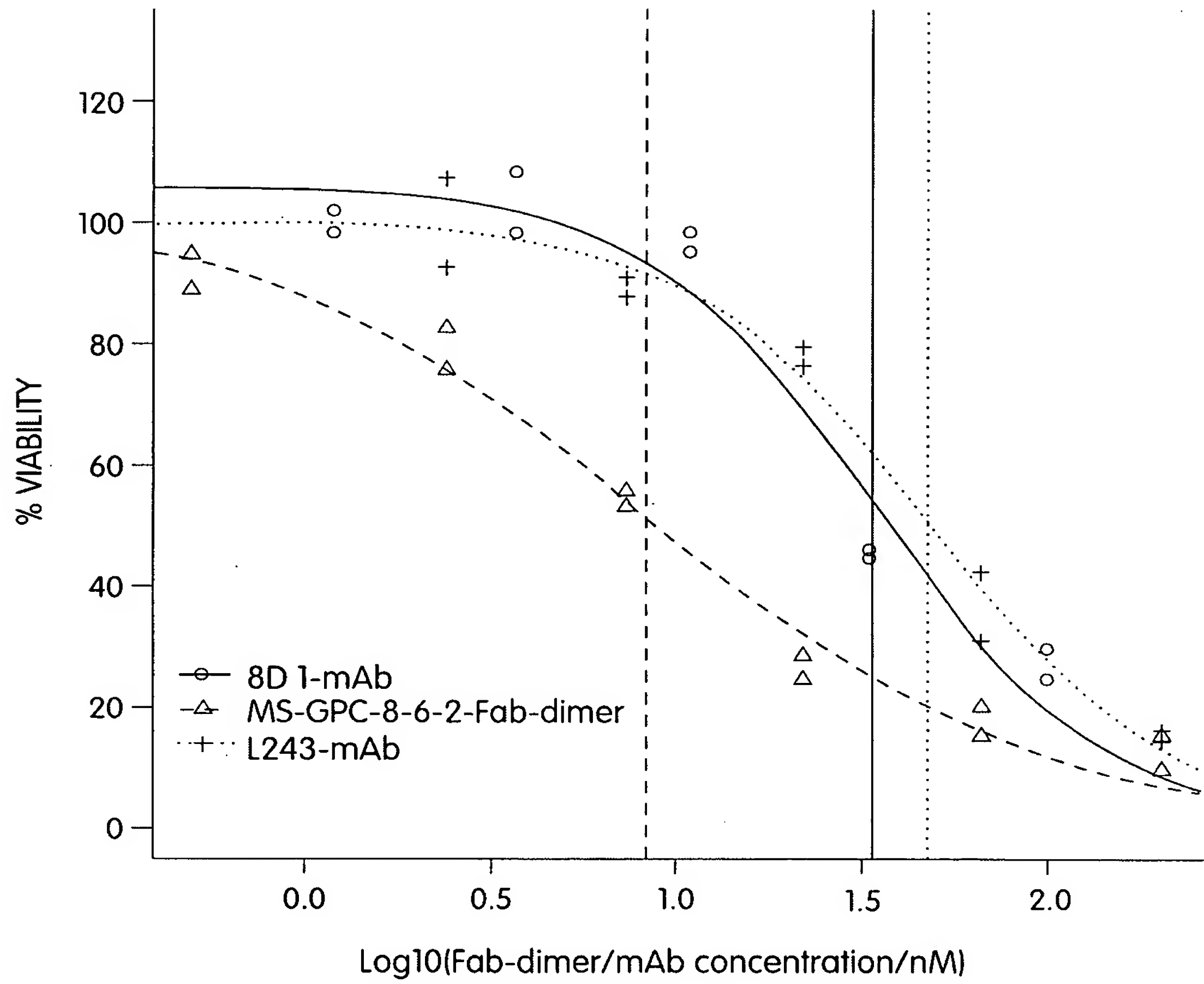


Fig. 7C

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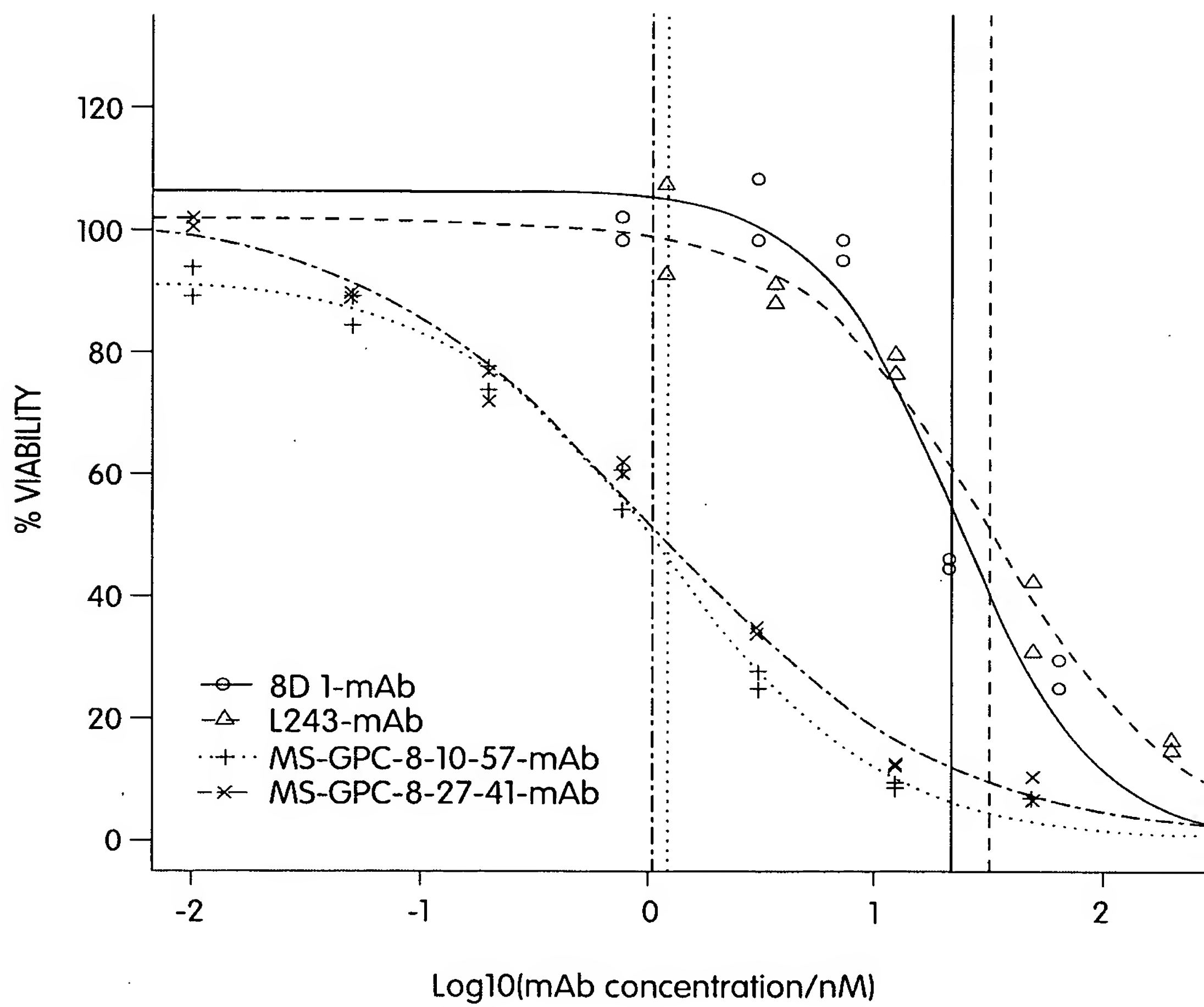


Fig. 7D

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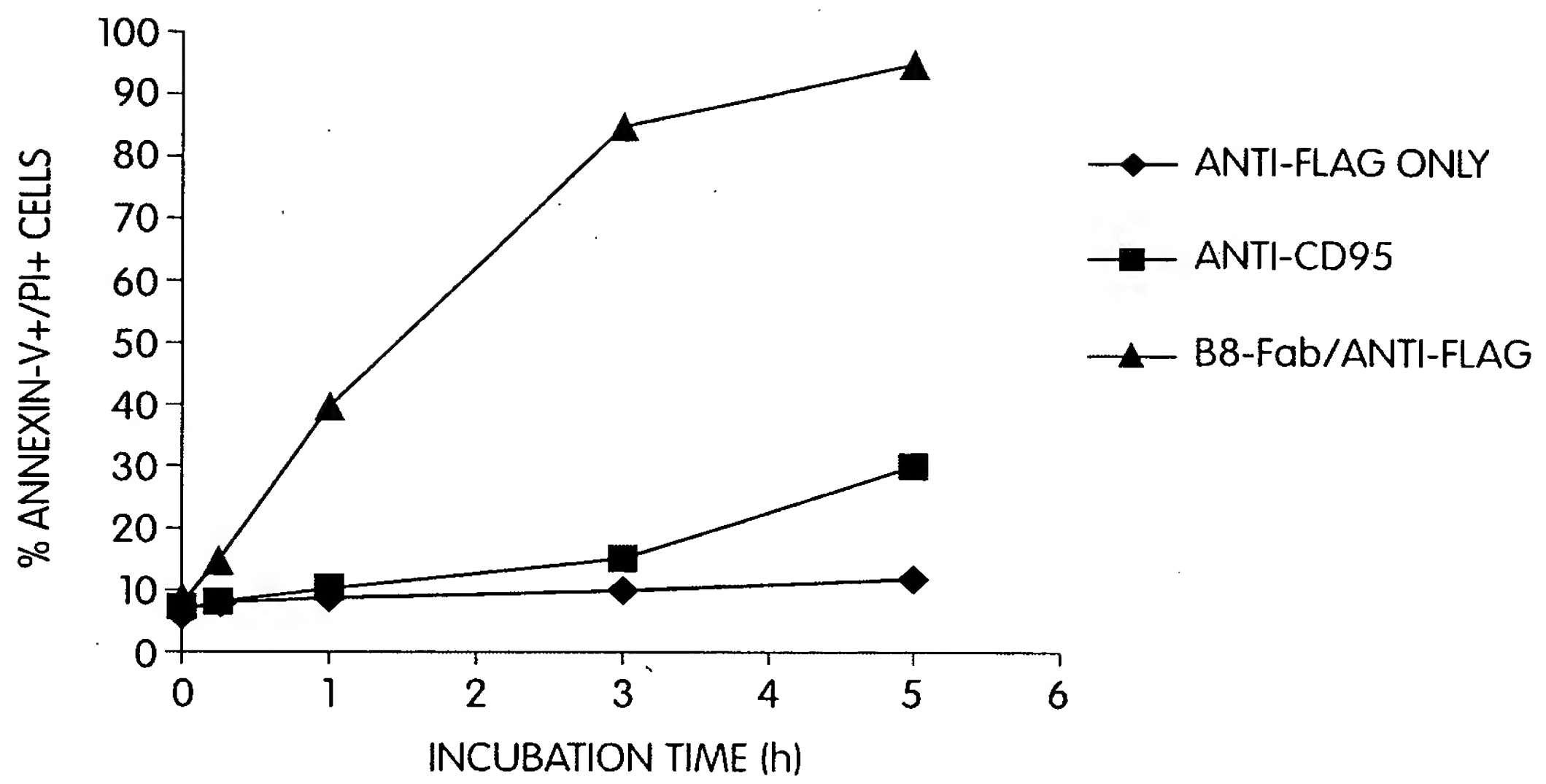


Fig. 8A

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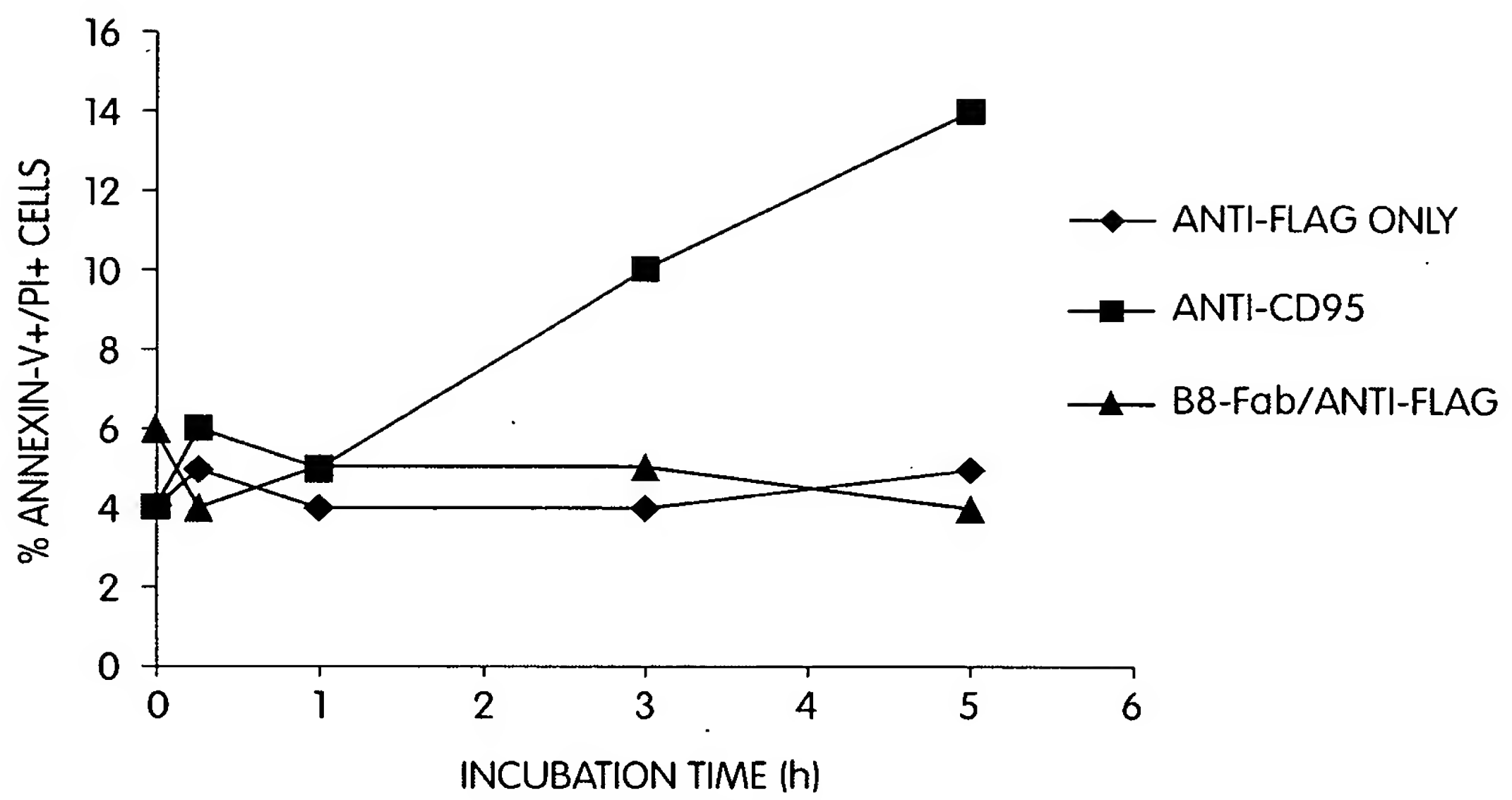


Fig. 8B



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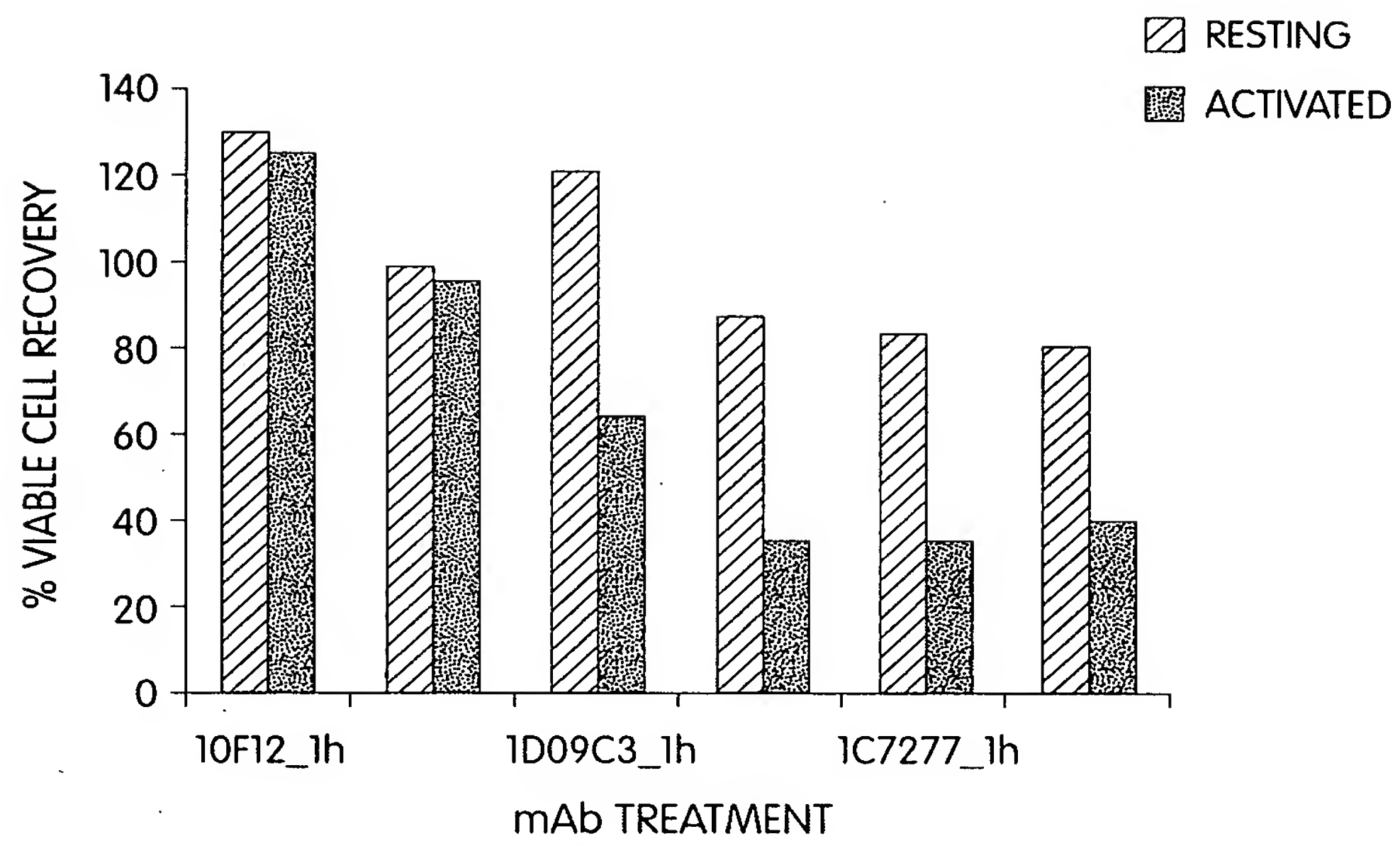


Fig. 8C

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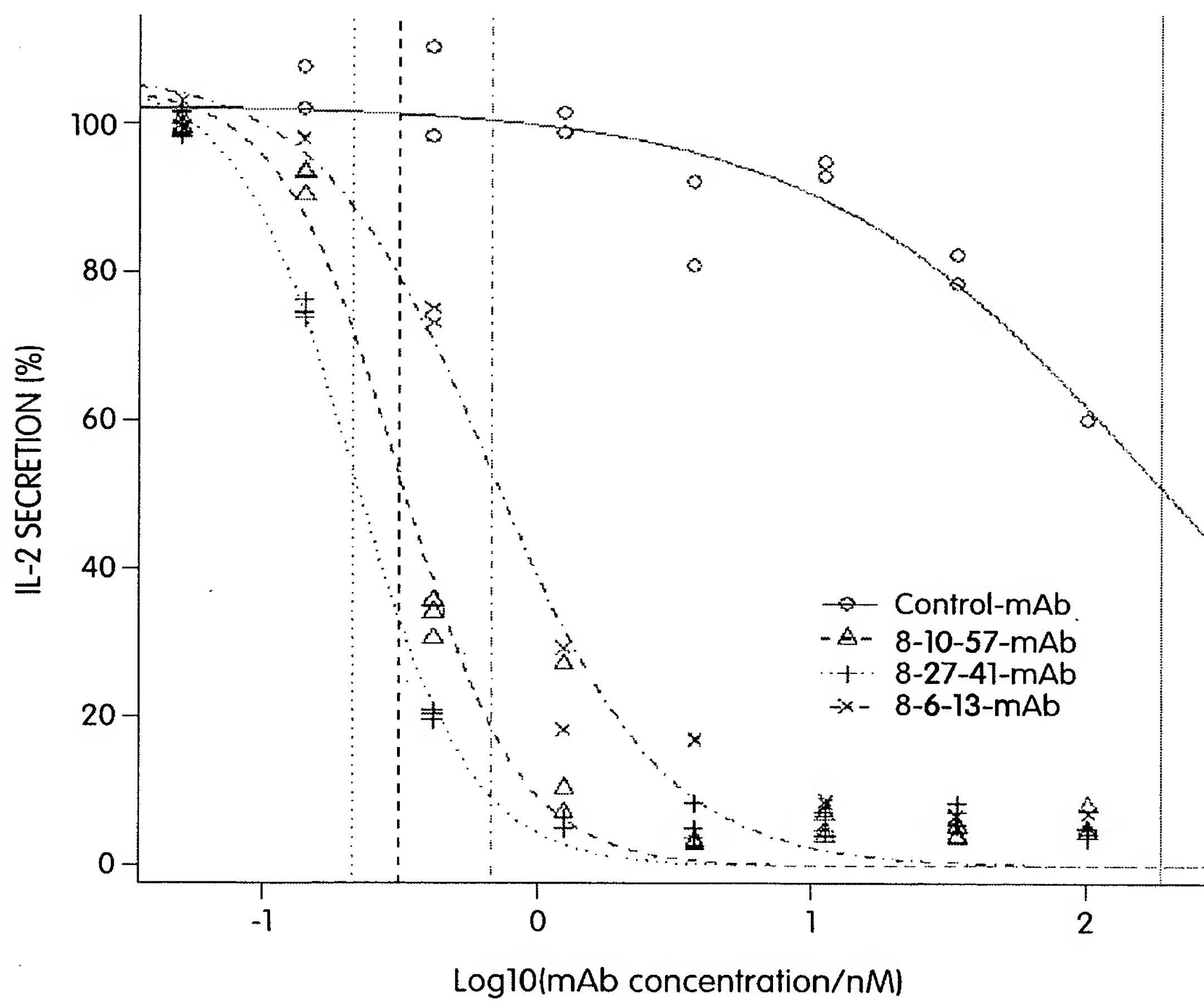


Fig. 9A

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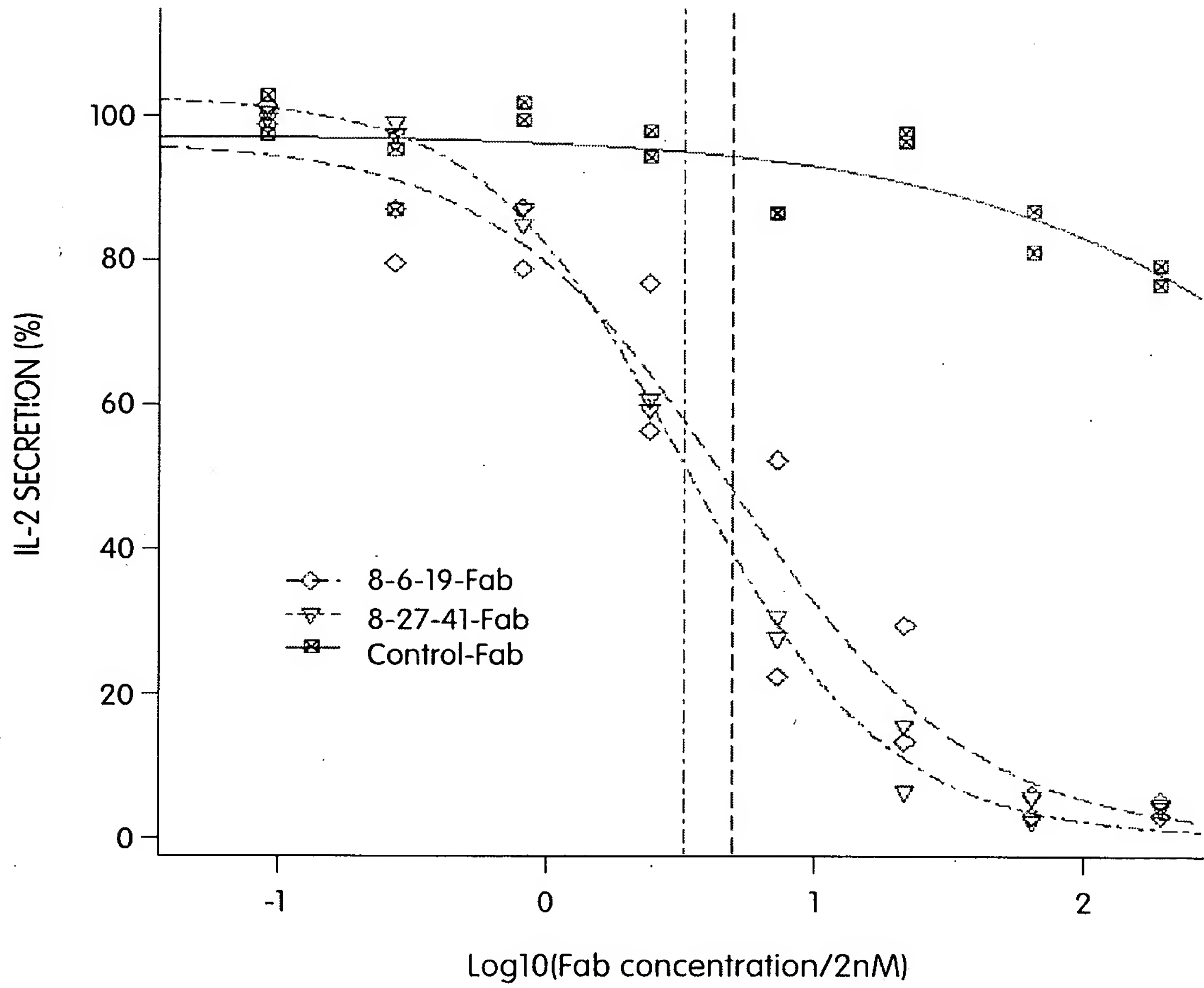
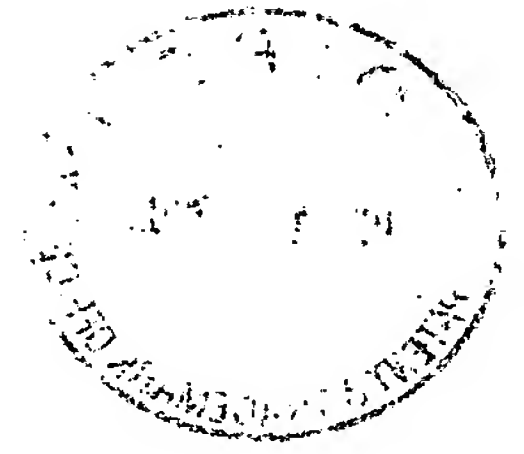


Fig. 9B

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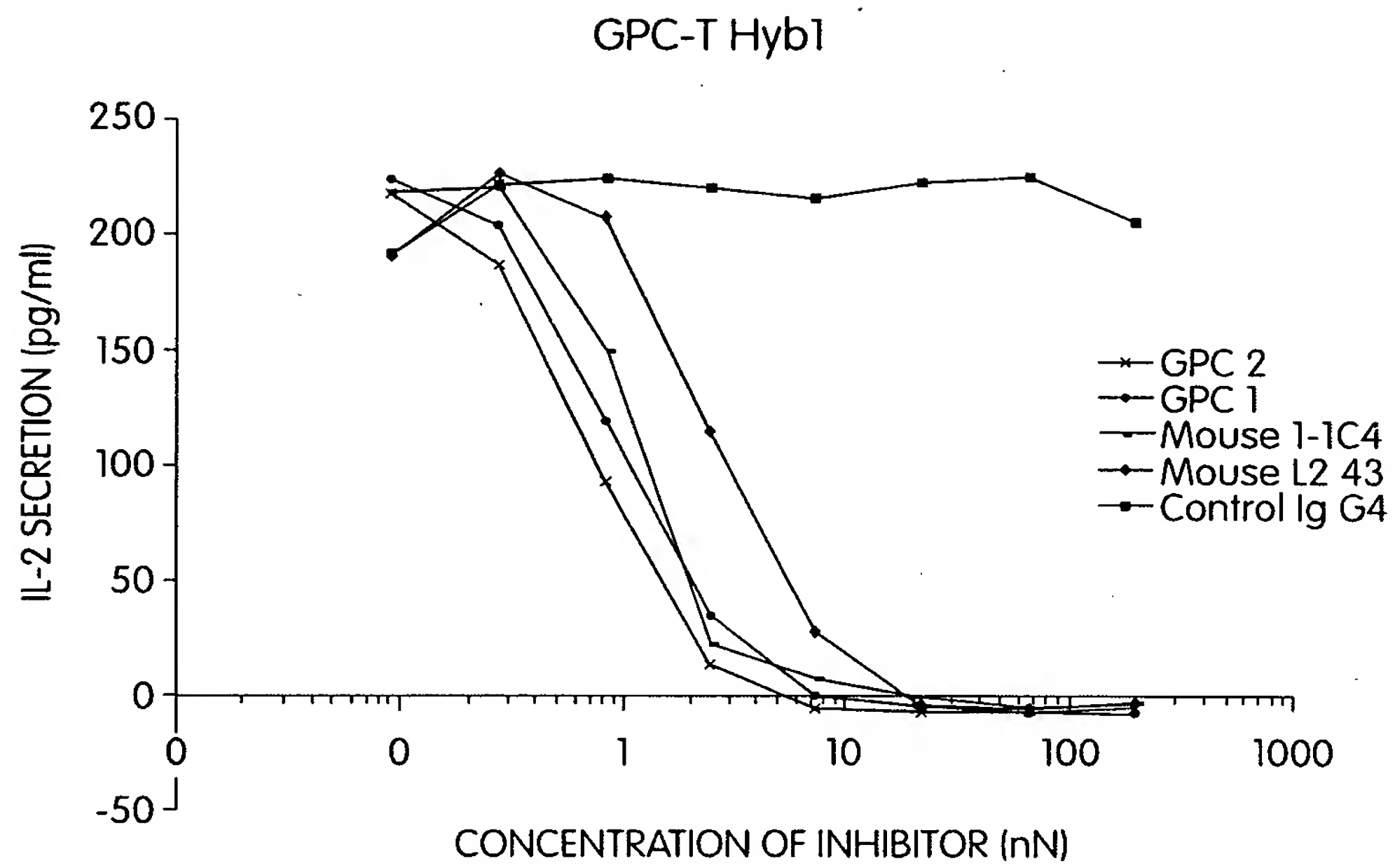
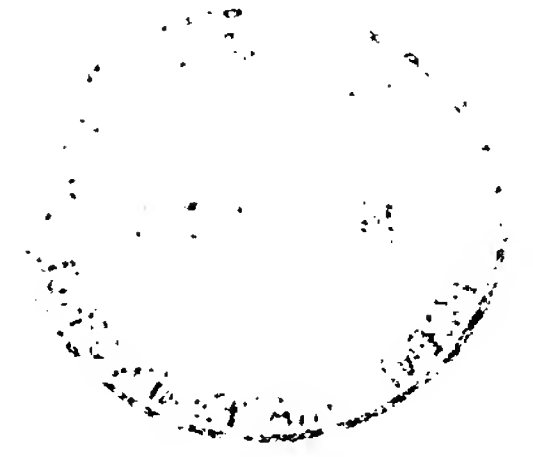


Fig. 9C

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Cell line NG-TcL HA-10

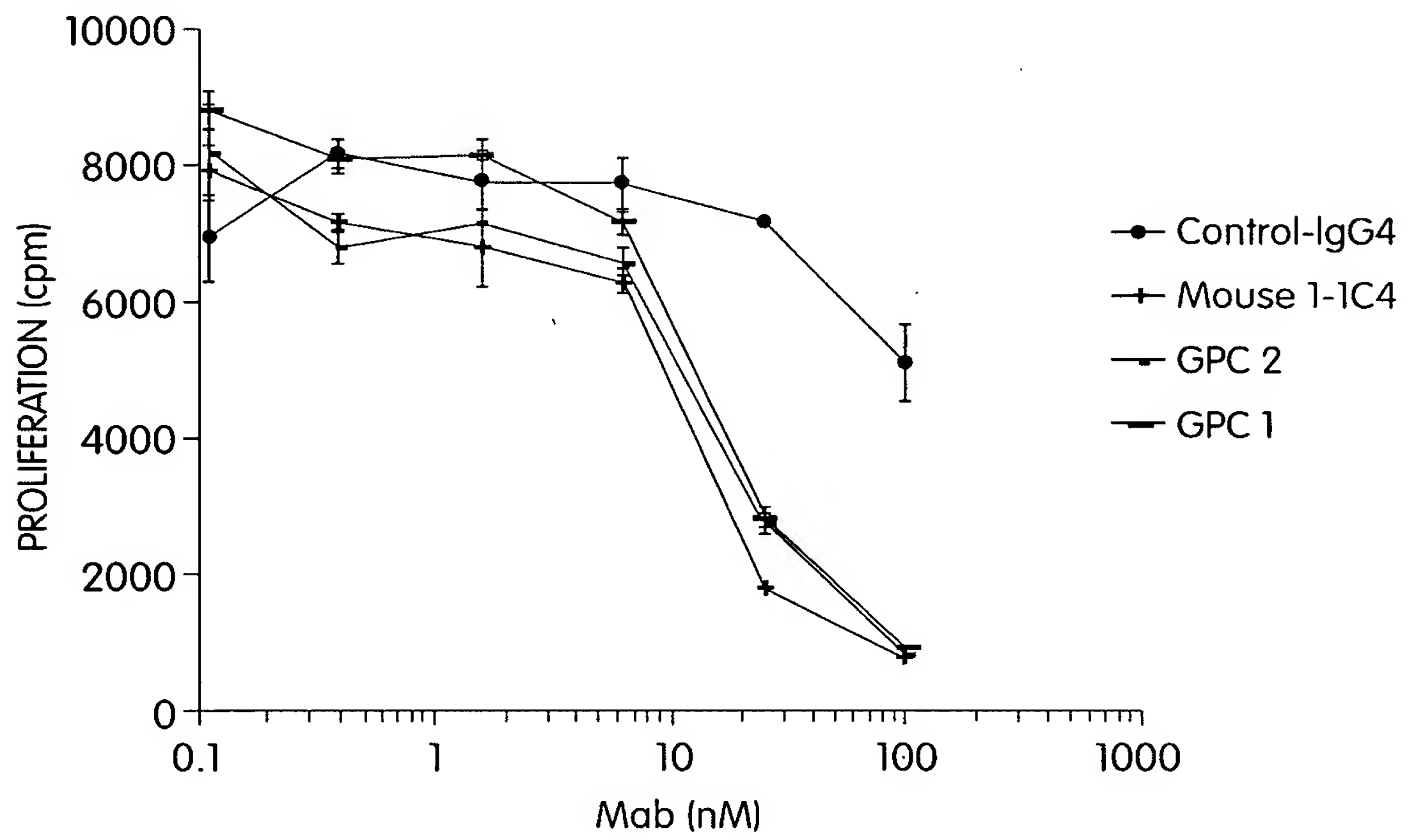


Fig. 9D

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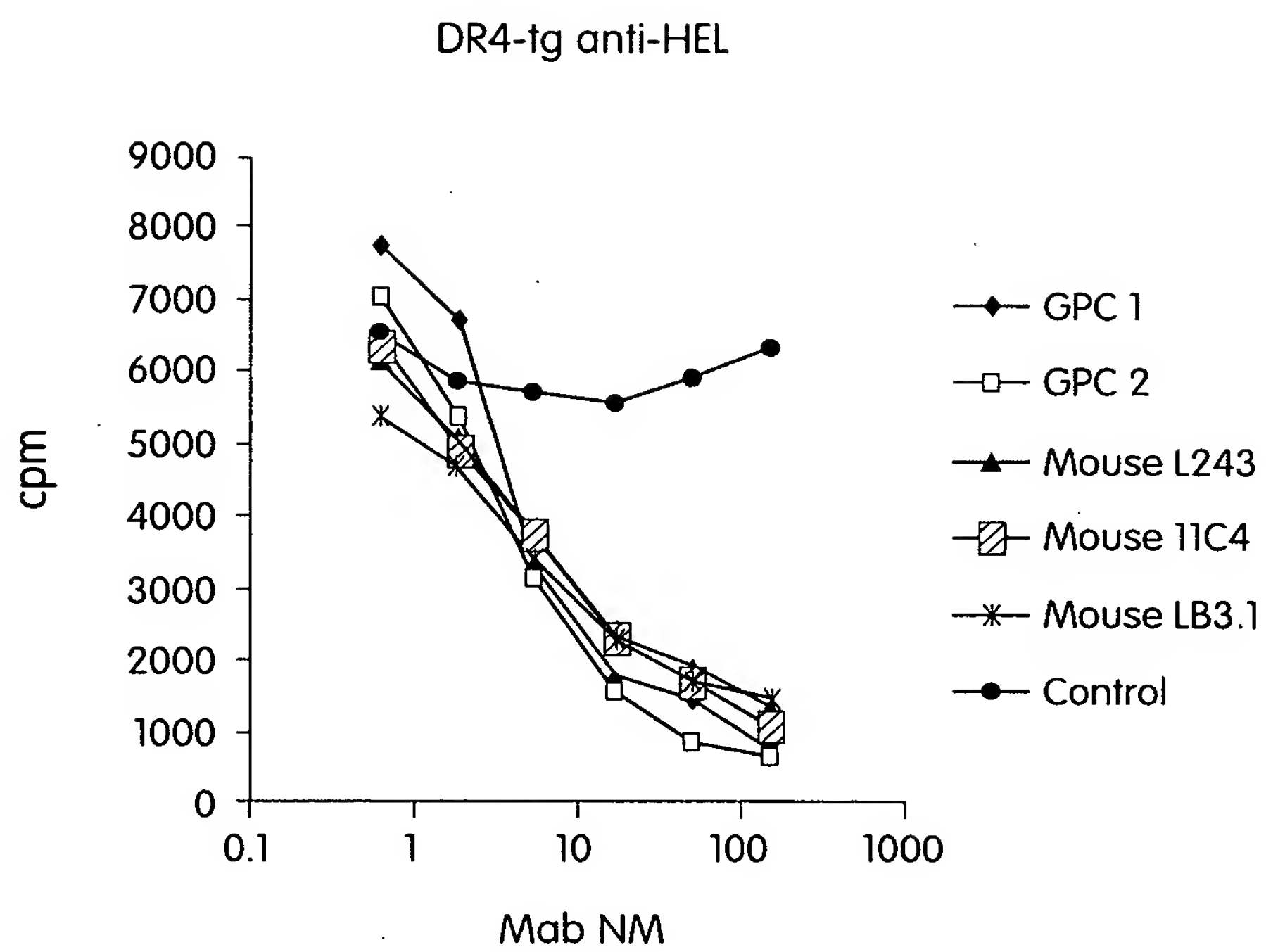


Fig. 9E

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DR14-tg anti-OVA

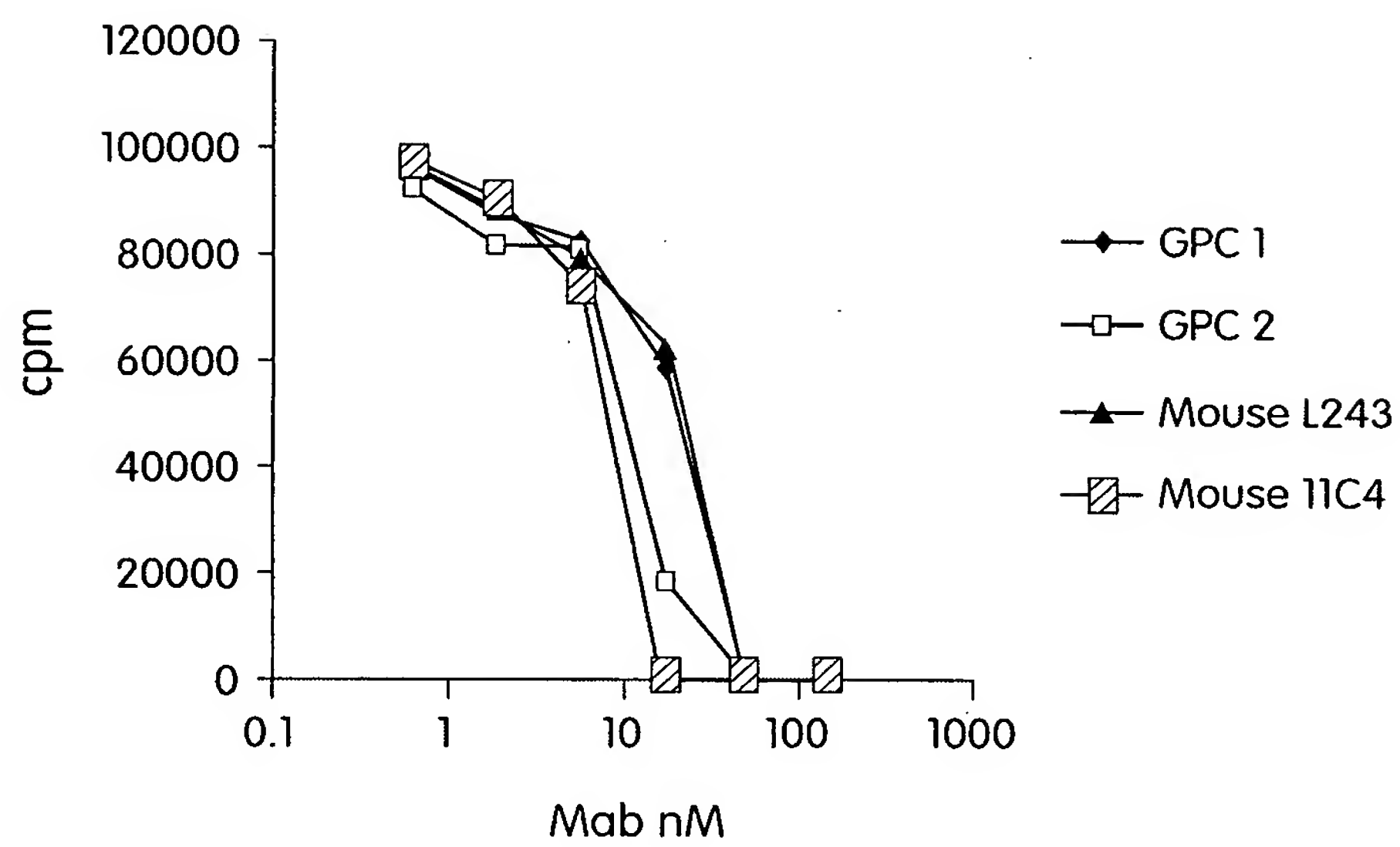


Fig. 9F

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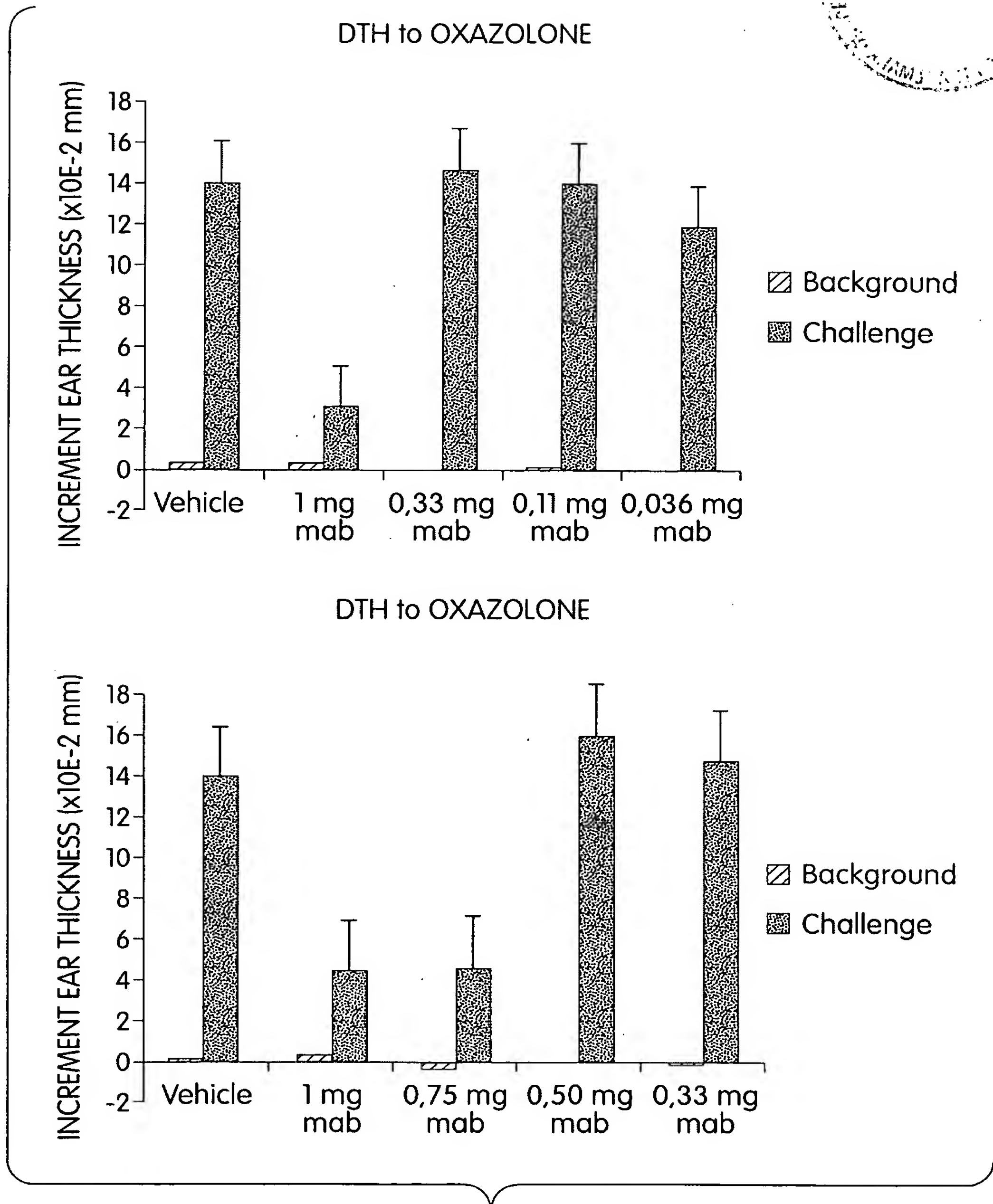
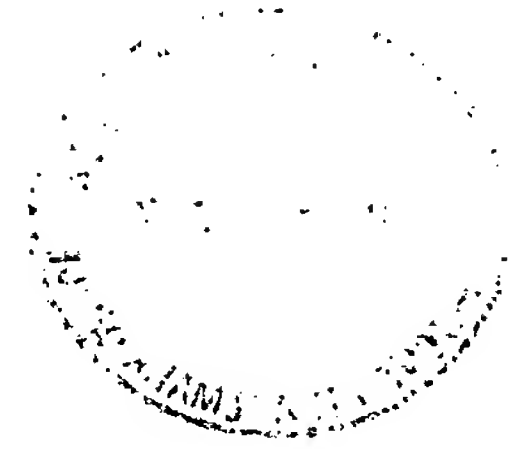


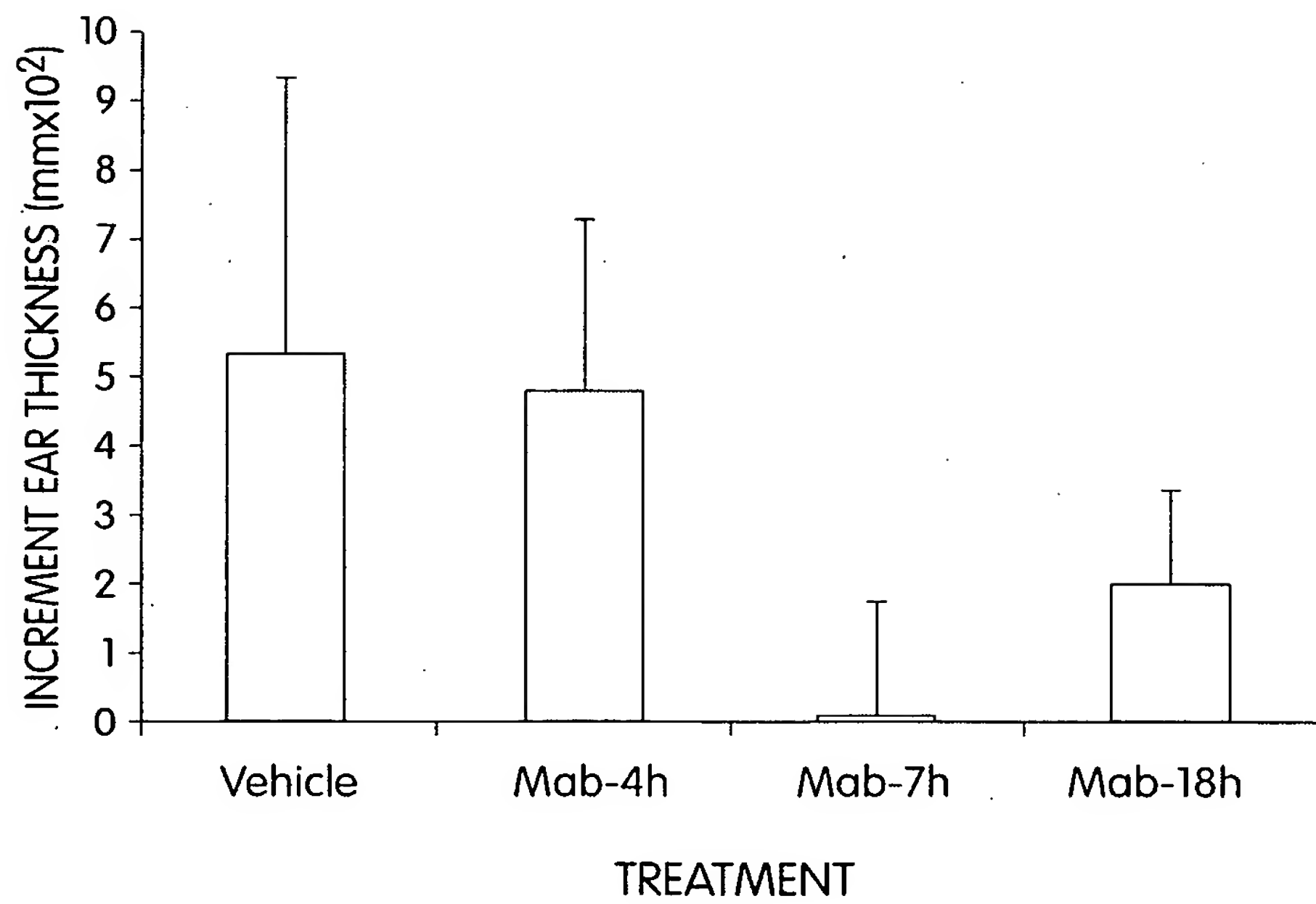
Fig. 9G



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DTH to DNFB



TREATMENT

Fig. 9H

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DTH to DNFB

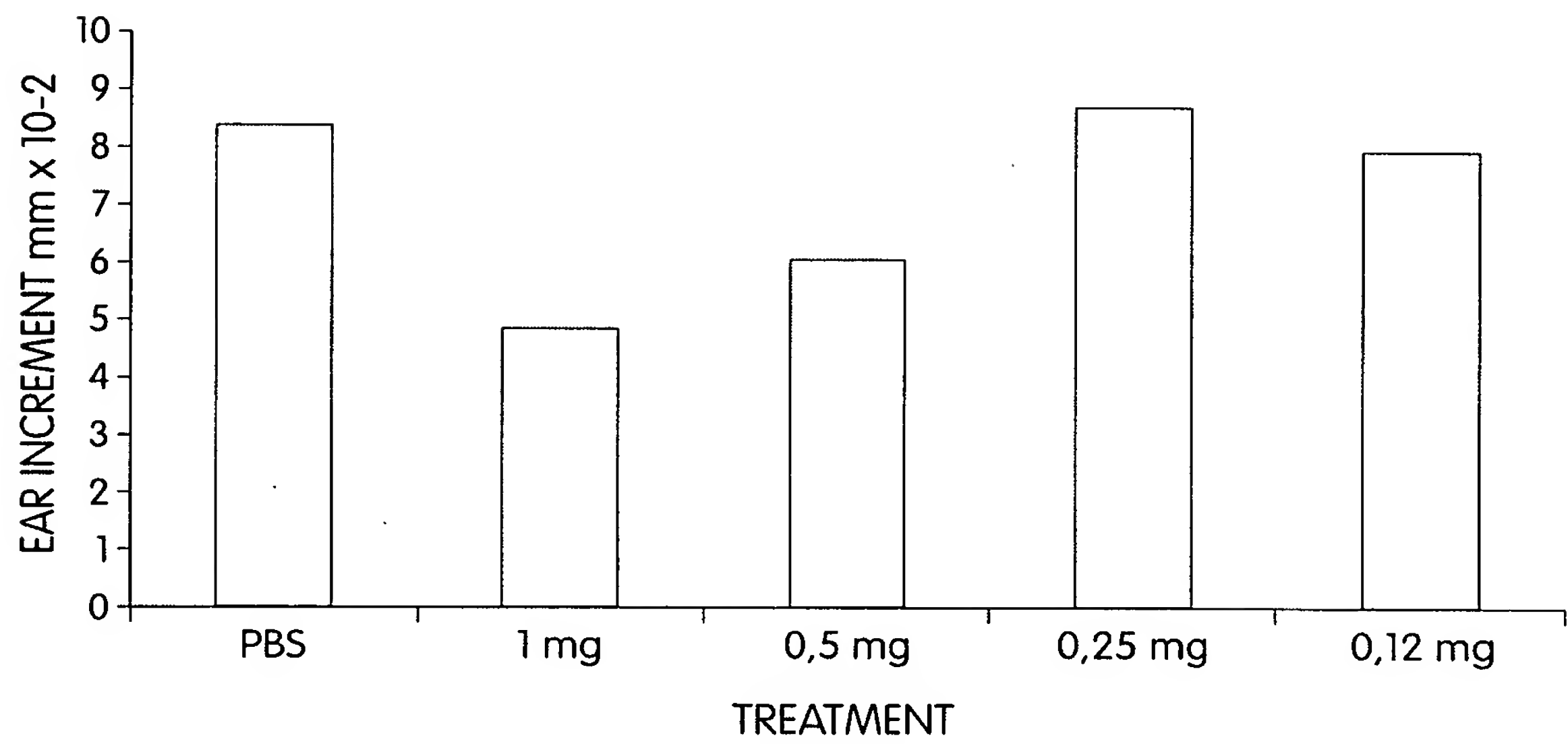


Fig. 9I

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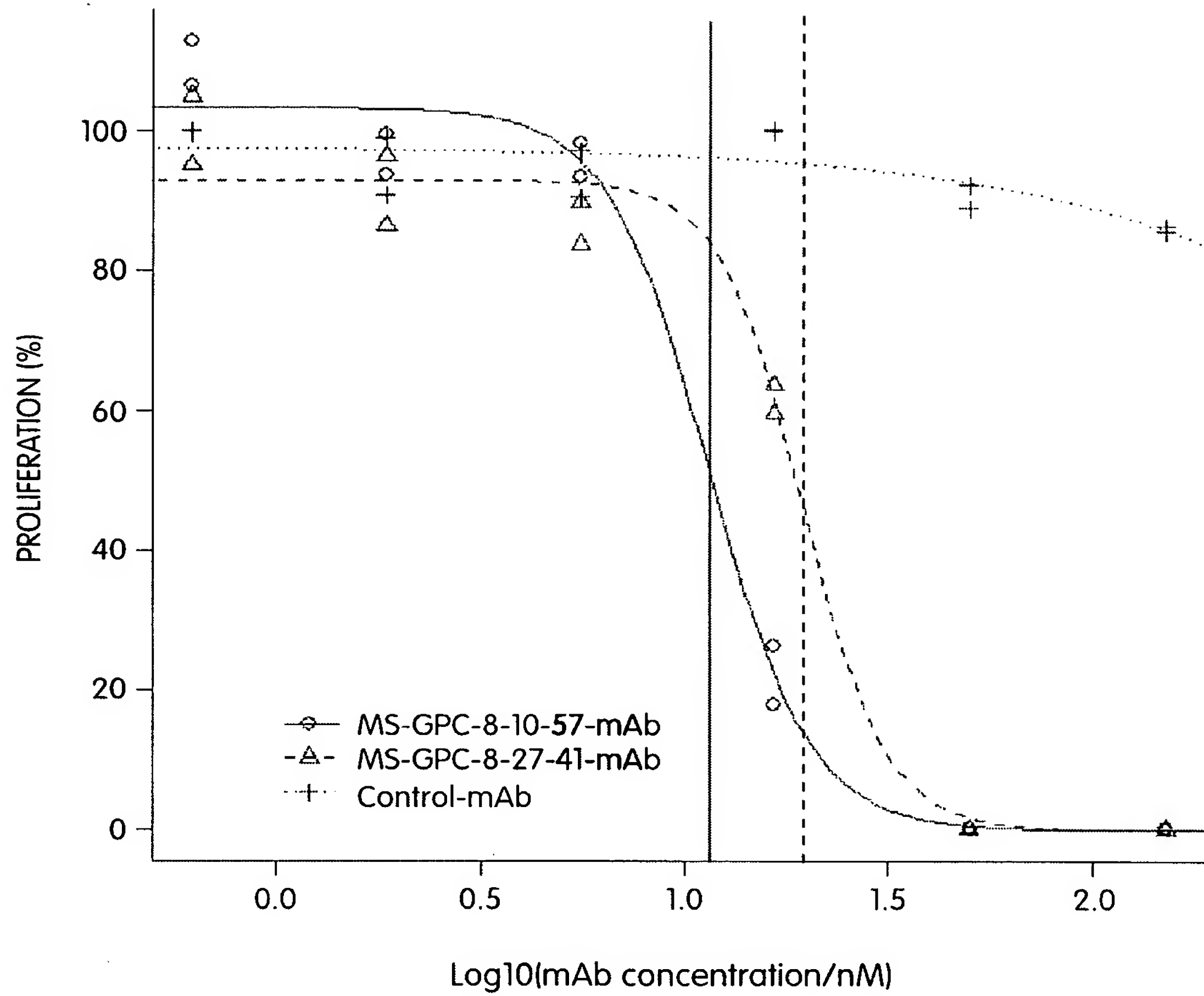


Fig. 10

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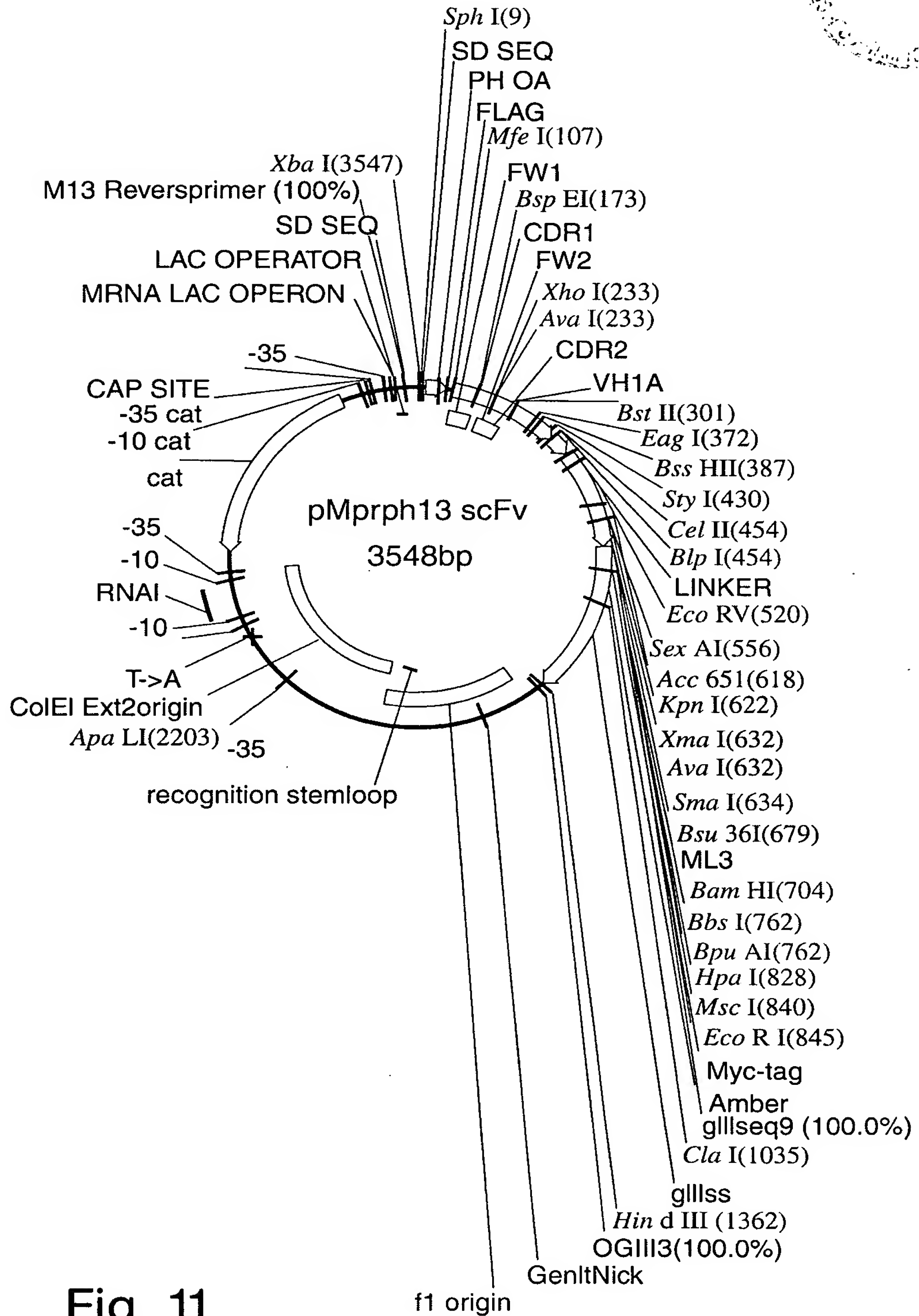



Fig. 11

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**XbaISphI**  
~~~~~

1 AGAGCATGCG TAGGAGAAAA TAAAATGAAA CAAAGCACTA TTGCACTGGC  
TCTCGTACGC ATCCTCTTTT ATTTTACTTT GTTTCGTGAT AACGTGACCG

51 ACTCTTACCG TTGCTCTTCA CCCCTGTTAC CAAAGCCGAC TACAAAGATG  
TGAGAATGGC AACGAGAAGT GGGGACAATG GTTTCGGCTG ATGTTTCTAC

**MfeI**  
~~~~~

101 AAGTGCAATT GGTTCACTCT GGCGCGGAAG TGAAAAAACC GGGCAGCAGC  
TTCACGTTAA CCAAGTCAGA CCGCGCCTTC ACTTTTTTTGG CCCGTCGTCG

**BspEI**  
~~~~~

151 GTGAAAGTGA GCTGCAAAGC CTCCGGAGGC ACTTTTAGCA GCTATGCGAT  
CACTTTCCTACT CGACGTTTCG GAGGCCTCCG TGAAAATCGT CGATACGCTA

**XhoI**  
~~~~~  
**AvaI**  
~~~~~

201 TAGCTGGGTG CGCCAAGCCC CTGGGCAGGG TCTCGAGTGG ATGGGCGGCA  
ATCGACCCAC GCGGTTTCGGG GACCCGTCCC AGAGCTCACC TACCCGCCGT

**BstEII**  
~

251 TTATTCCGAT TTTTGGCACG GCGAACTACG CGCAGAAGTT TCAGGGCCGG  
AATAAGGCTA AAAACCGTGC CGCTTGATGC GCGTCTTCAA AGTCCCGGCC

**BstEII**  
~~~~~

301 GTGACCATTA CCGCGGATGA AAGCACCAGC ACCGCGTATA TGGAAGTGA  
CACTGGTAAT GGCGCCTACT TTCGTGGTCG TGGCGCATAT ACCTTGACTC

**EagI**                      **BssHII**  
~~~~~                      ~~~~~

351 CAGCCTGCGT AGCGAAGATA CGGCCGTGTA TTATTGCGCG CGTTATTATG  
GTCGGACGCA TCGCTTCTAT GCCGGCACAT AATAACGCGC GCAATAATAC

**StyI**  
~~~~~

401 ATCGTATGTA TAATATGGAT TATTGGGGCC AAGGCACCCT GGTGACGGTT  
TAGCATAACAT ATTATACCTA ATAACCCCGG TTCCGTGGGA CCACTGCCAA

**BlpI**  
~~~~~  
**CelII**  
~~~~~

451 AGCTCAGCGG GTGGCGGTTT TGGCGGCGGT GGGAGCGGTG GCGGTGGTTC

Fig. 11 (cont.)

Fig. 11 (cont.)

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CTGGCTTTTA CGGCTACTTT TGC GCGATGT CAGACTGCGA TTTCCGTTTG

ClaI

~~~~~

1001 TTGATTCTGT CGCTACTGAT TACGGTGCTG CTATCGATGG TTTCAATTGGT  
 AACTAAGACA GCGATGACTA ATGCCACGAC GATAGCTACC AAAGTAACCA

1051 GACGTTTCCG GCCTTGCTAA TGGTAATGGT GCTACTGGTG ATTTTGCTGG  
 CTGCAAAGGC CGGAACGATT ACCATTACCA CGATGACCAC TAAAACGACC

1101 CTCTAATTCC CAAATGGCTC AAGTCGGTGA CGGTGATAAT TCACCTTTAA  
 GAGATTAAGG GTTTACCGAG TTCAGCCACT GCCACTATTA AGTGGAATT

1151 TGAATAATTT CCGTCAATAT TTACCTTCCC TCCCTCAATC GGTGGAATGT  
 ACTTATTAAA GGCAGTTATA AATGGAAGGG AGGGAGTTAG CCAACTTACA

1201 CGCCCTTTTG TCTTTGGCGC TGGTAAACCA TATGAATTTT CTATTGATTG  
 GCGGGAAAAC AGAAACCGCG ACCATTTGGT ATACTTAAAA GATAACTAAC

1251 TGACAAAATA AACTTATTCC GTGGTGTCTT TCGGTTTCTT TTATATGTTG  
 ACTGTTTTAT TTGAATAAGG CACCACAGAA ACGCAAAGAA AATATACAAC

1301 CCACCTTTAT GSTATGTATTT TCTACGTTTG CTAACATACT GCGTAATAAG  
 GGTGGAATA CATACATAAA AGATGCAAAC GATTGTATGA CGCATTATTC

HindIII

~~~~~

1351 GAGTCTTGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG  
 CTCAGAACTA TTCGAACTGG ACACTTCACT TTTTACCGCG TCTAACACGC

OGIII3 100.0%

=====

1401 ACATTTTTTTT TGTCTGCCGT TTAATGAAAT TGTAACCGTT AATATTTTGT  
 TGTAACAAAA ACAGACGGCA AATTACTTTA ACATTTGCAA TTATAAAACA

1451 TAAAATTCGC GTTAAATTTT TGTAAATCA GCTCATTTTT TAACCAATAG  
 ATTTTAAGCG CAATTTAAAA ACAATTTAGT CGAGTAAAA ATTGGTTATC

1501 GCCGAAATCG GCAAAATCCC TTATAAATCA AAAGAATAGA CCGAGATAGG  
 CGGCTTTAGC CGTTTTAGGG AATATTTAGT TTTCTTATCT GGCTCTATCC

1551 GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG  
 CAACTCACAA CAAGGTCAAA CCTTGTTCTC AGGTGATAAT TTCTTGCACC

1601 ACTCCAACGT CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA  
 TGAGGTTGCA GTTTCCCGCT TTTTGGCAGA TAGTCCCGCT ACCGGGTGAT

1651 CGAGAACCAT CACCCTAATC AAGTTTTTTT GGGTCGAGGT GCCGTAAAGC  
 GCTCTTGGTA GTGGGATTAG TTCAAAAAAC CCCAGCTCCA CGGCATTTCG

1701 ACTAAATCGG AACCTTAAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA  
 TGATTTAGCC TTGGGATTTC CCTCGGGGGC TAAATCTCGA ACTGCCCTT

Fig. 11 (cont.)

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1751	AGCCGGCGAA	CGTGGCGAGA	AAGGAAGGGA	AGAAAGCGAA	AGGAGCGGGC
	TCGGCCGCTT	GCACCGCTCT	TTCCTTCCCT	TCTTTCGCTT	TCCTCGCCCC
1801	GCTAGGGCGC	TGGCAAGTGT	AGCGGTCACG	CTGCGCGTAA	CCACCACACC
	CGATCCCCGCG	ACCGTTCACA	TCGCCAGTGC	GACGCGCATT	GGTGGTGTGG
1851	CGCCGCGCTT	AATGCGCCGC	TACAGGGCGC	GTGCTAGCCA	TGTGAGCAAA
	GCGGCGCGAA	TTACGCGGCG	ATGTCCCGCG	CACGATCGGT	ACACTCGTTT
1901	AGGCCAGCAA	AAGGCCAGGA	ACCGTAAAAA	GGCCGCGTTG	CTGGCGTTTT
	TCCGGTCGTT	TTCCGGTCCT	TGGCATTTTT	CCGGCGCAAC	GACCGCAAAA
1951	TCCATAGGCT	CCGCCCCCCT	GACGAGCATC	ACAAAAATCG	ACGCTCAAGT
	AGGTATCCGA	GGCGGGGGGA	CTGCTCGTAG	TGTTTTTAGC	TGCGAGTTCA
2001	CAGAGGTGGC	GAAACCCGAC	AGGACTATAA	AGATACCAGG	CGTTTCCCCC
	GTCTCCACCG	CTTTGGGCTG	TCCTGATATT	TCTATGGTCC	GCAAAGGGGG
2051	TGGAAGCTCC	CTCGTGCCT	CTCCTGTTCC	GACCTTGCCG	CTTACCGGAT
	ACCTTCGAGG	GAGCACGCGA	GAGGACAAGG	CTGGGACGGC	GAATGGCCTA
2101	ACCTGTCCGC	CTTTCTCCCT	TCGGGAAGCG	TGGCGCTTTC	TCATAGCTCA
	TGGACAGGCG	GAAAGAGGGA	AGCCCTTCGC	ACCGCGAAAG	AGTATCGAGT
2151	CGCTGTAGGT	ATCTCAGTTC	GGTGTAGGTC	GTTCGCTCCA	AGCTGGGCTG
	GCGACATCCA	TAGAGTCAAG	CCACATCCAG	CAAGCGAGGT	TCGACCCGAC
	ApaLI				
	~~~~~				
2201	TGTGCACGAA	CCCCCGGTTT	AGTCCGACCG	CTGCGCCTTA	TCCGGTAACT
	ACACGTGCTT	GGGGGGCAAG	TCAGGCTGGC	GACGCGGAAT	AGGCCATTGA
2251	ATCGTCTTGA	GTCCAACCCG	GTAAGACACG	ACTTATCGCC	ACTGGCAGCA
	TAGCAGAACT	CAGGTTGGGC	CATTCTGTGC	TGAATAGCGG	TGACCGTCGT
2301	GCCACTGGTA	ACAGGATTAG	CAGAGCGAGG	TATGTAGGCG	GTGCTACAGA
	CGGTGACCAT	TGTCCTAATC	GTCTCGCTCC	ATACATCCGC	CACGATGTCT
2351	GTTCTTGAAG	TGGTGGCCTA	ACTACGGCTA	CACTAGAAGA	ACAGTATTTG
	CAAGAACTTC	ACCACCGGAT	TGATGCCGAT	GTGATCTTCT	TGTCATAAAC
2401	GTATCTGCGC	TCTGCTGTAG	CCAGTTACCT	TCGGAAAAAG	AGTTGGTAGC
	CATAGACGCG	AGACGACATC	GGTCAATGGA	AGCCTTTTTC	TCAACCATCG
2451	TCTTGATCCG	GCAAACAAAC	CACCGCTGGT	AGCGGTGGTT	TTTTTGTTTG
	AGAACTAGGC	CGTTTGTTTG	GTGGCGACCA	TCGCCACCAA	AAAAACAAAC
2501	CAAGCAGCAG	ATTACGCGCA	GAAAAAAAGG	ATCTCAAGAA	GATCCTTTGA
	GTTGTCGTC	TAATGCGCGT	CTTTTTTTTC	TAGAGTTCTT	CTAGGAAACT
2551	TCTTTTCTAC	GGGGTCTGAC	GCTCAGTGGA	ACGAAAACTC	ACGTTAAGGG

Fig. 11 (cont.)



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	AGAAAAGATG	CCCCAGACTG	CGAGTCACCT	TGCTTTTGAG	TGCAATTCCC
2601	ATTTTGGTCA TAAAACCAGT	GATCTAGCAC CTAGATCGTG	CAGGCGTTTA GTCCGCAAAT	AGGGCACCAA TCCCGTGGTT	TAACTGCCTT ATTGACGGAA
2651	AAAAAATTA TTTTTTTAAT	CGCCCCGCCC GCGGGGCGGG	TGCCACTCAT ACGGTGAGTA	CGCAGTACTG GCGTCATGAC	TTGTAATTCA AACATTAAGT
2701	TTAAGCATT AATTCGTAAG	TGCCGACATG ACGGCTGTAC	GAAGCCATCA CTTCGGTAGT	CAAACGGCAT GTTTGCCGTA	GATGAACCTG CTACTTGGAC
2751	AATCGCCAGC TTAGCGGTCG	GGCATCAGCA CCGTAGTCGT	CCTTGTCGCC GGAACAGCGG	TTGCGTATAA AACGCATATT	TATTTGCCCA ATAAACGGGT
2801	TAGTGAAAAC ATCACTTTTG	GGGGGCGAAG CCCCCGCTTC	AAGTTGTCCA TTCAACAGGT	TATTGGCTAC ATAACCGATG	GTTTAAATCA CAAATTTAGT
2851	AAACTGGTGA TTTGACCACT	AACTCACCCA TTGAGTGGGT	GGGATTGGCT CCCTAACCGA	GAGACGAAAA CTCTGCTTTT	ACATATTCTC TGTATAAGAG
2901	AATAAACCCCT TTATTTGGGA	TTAGGGAAAT AATCCCTTTA	AGGCCAGGTT TCCGGTCCAA	TTCACCGTAA AAGTGGCATT	CACGCCACAT GTGCGGTGTA
2951	CTTGCGAATA GAACGCTTAT	TATGTGTAGA ATACACATCT	AACTGCCGGA TTGACGGCCT	AATCGTCGTG TTAGCAGCAC	GTATTCACTC CATAAGTGAG
3001	CAGAGCGATG GTCTCGCTAC	AAAACGTTTC TTTTGCAAAG	AGTTTGCTCA TCAAACGAGT	TGGAAAACGG ACCTTTTGCC	TGTAACAAGG ACATTGTTCC
3051	GTGAACACTA CACTTGTGAT	TCCCATATCA AGGGTATAGT	CCAGCTCACC GGTCGAGTGG	GTCTTTCATT CAGAAAGTAA	GCCATACGGA CGGTATGCCT
3101	ACTCCGGGTG TGAGGCCAC	AGCATTCATC TCGTAAGTAG	AGGCGGGCAA TCCGCCCGTT	GAATGTGAAT CTTACACTTA	AAAGGCCGGA TTTCCGGCCT
3151	TAAAACTTGT ATTTTGAACA	GCTTATTTTT CGAATAAAAA	CTTTACGGTC GAAATGCCAG	TTTAAAAAGG AAATTTTTC	CCGTAATATC GGCATTATAG
3201	CAGCTGAACG GTCGACTTGC	GTCTGGTTAT CAGACCAATA	AGGTACATTG TCCATGTAAC	AGCAACTGAC TCGTTGACTG	TGAAATGCCT ACTTTACGGA
3251	CAAAATGTTC GTTTTACAAG	TTTACGATGC AAATGCTACG	CATTGGGATA GTAACCCTAT	TATCAACGGT ATAGTTGCCA	GGTATATCCA CCATATAGGT
3301	GTGATTTTTT CACTAAAAAA	TCTCCATTTT AGAGGTAAAA	AGCTTCCTTA TCGAAGGAAT	GCTCCTGAAA CGAGGACTTT	ATCTCGATAA TAGAGCTATT
3351	CTCAAAAAAT GAGTTTTTTA	ACGCCCCGTA TGCGGGCCAT	GTGATCTTAT CACTAGAATA	TTCATTATGG AAGTAATACC	TGAAAGTTGG ACTTTCAACC
3401	AACCTCACCC TTGGAGTGGG	GACGTCTAAT CTGCAGATTA	GTGAGTTAGC CACTCAATCG	TCACTCATTA AGTGAGTAAT	GGCACCCCAG CCGTGGGGTC

Fig. 11 (cont.)

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3451 GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG  
CGAAATGTGA AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC

M13 Reverse primer 100.0%

XbaI

=====

3501 ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GAATTTCT  
TATTGTTAAA GTGTGTCCTT TGTCGATACT GGTACTAATG CTTAAAGA

Fig. 11 (cont.)

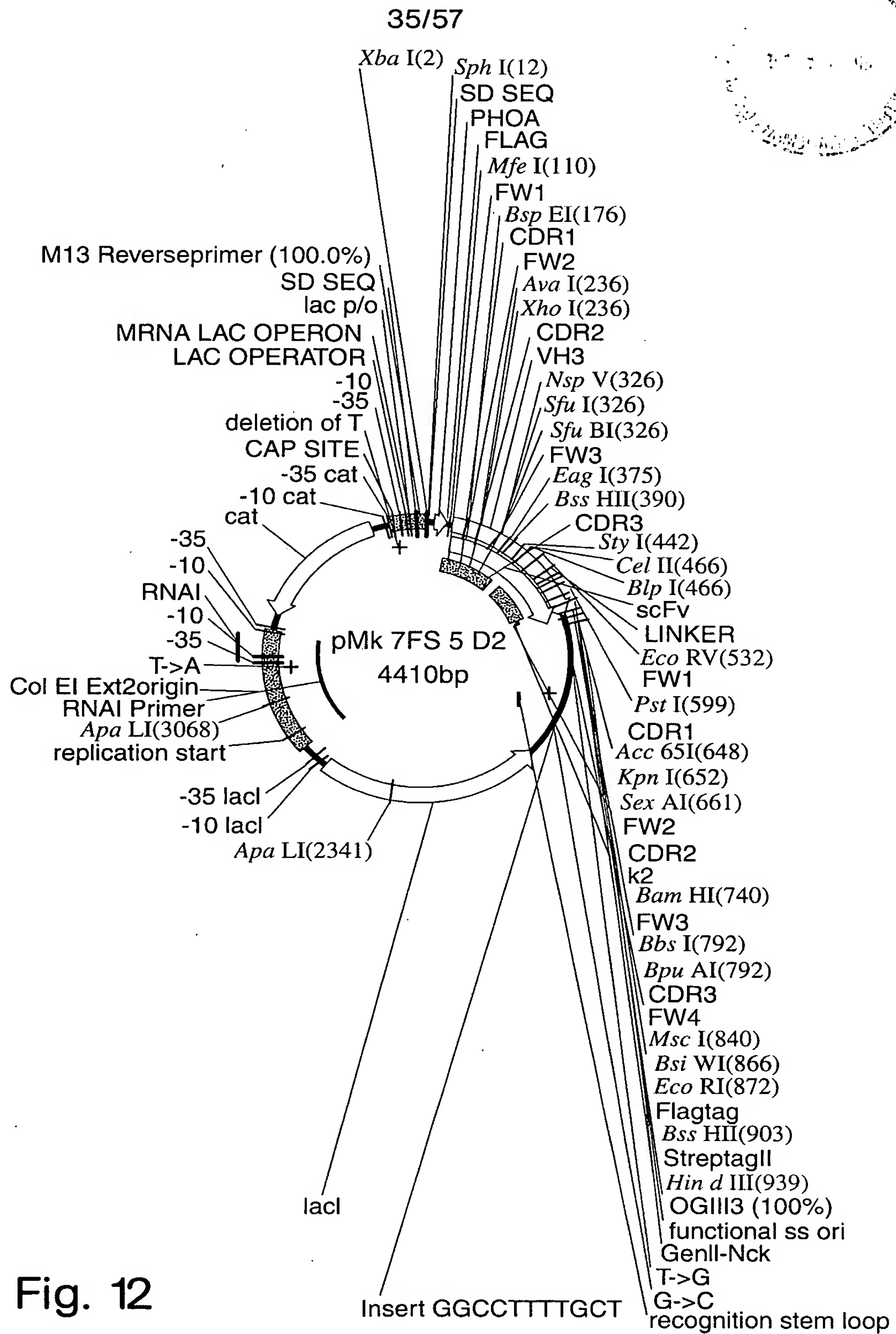


Fig. 12

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XbaI SphI  
~~~~~

1 TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAAGCA CTATTGCACT  
AGATCTCGTA CGCATCCTCT TTTATTTTAC TTTGTTTCGT GATAACGTGA

51 GGCACCTCTTA CCGTTGCTCT TCACCCCTGT TACCAAAGCC GACTACAAAG  
CCGTGAGAAT GGCAACGAGA AGTGGGGACA ATGGTTTCGG CTGATGTTTC

MfeI  
~~~~~

101 ATGAAGTGCA ATTGGTGGAA AGCGGCGGCG GCCTGGTGCA ACCGGGCGGC  
TACTTCACGT TAACCACCTT TCGCCGCCGC CGGACCACGT TGGCCCGCCG

BspEI  
~~~~~

151 AGCCTGCGTC TGAGCTGCGC GGCCTCCGGA TTTACCTTTA GCAGCTATGC  
TCGGACGCAG ACTCGACGCG CCGGAGGCCT AAATGGAAAT CGTCGATACG

XhoI  
~~~~~  
AvaI  
~~~~~

201 GATGAGCTGG GTGCGCCAAG CCCCTGGGAA GGGTCTCGAG TGGGTGAGCG  
CTACTCGACC CACGCGGTTC GGGGACCCTT CCCAGAGCTC ACCCACTCGC

251 CGATTAGCGG TAGCGGCGGC AGCACCTATT ATGCGGATAG CGTGAAAGGC  
GCTAATCGCC ATCGCCGCCG TCGTGGATAA TACGCCTATC GCACTTTCCG

BstBI  
~~~~~  
SfuI  
~~~~~  
NspV  
~~~~~

301 CGTTTTACCA TTTCACGTGA TAATTCGAAA AACACCCTGT ATCTGCAAAT  
GCAAAATGGT AAAGTGCACT ATTAAGCTTT TTGTGGGACA TAGACGTTTA

EagI  
~~~~~  
BssHII  
~~~~~

351 GAACAGCCTG CGTGCGGAAG ATACGGCCGT GTATTATTGC GCGCGTGTTA  
CTTGTCGGAC GCACGCCTTC TATGCCGGCA CATAATAACG CGCGCACAAAT

StyI  
~~~~~

401 AGAAGCATTT TTCTCGTAAG AATTGGTTTG ATTATTGGGG CCAAGGCACC  
TCTTCGTAAA AAGAGCATTC TTAACCAAAC TAATAACCCC GGTTCCGTGG

Fig. 12 (cont.)



Fig. 12 (cont.)

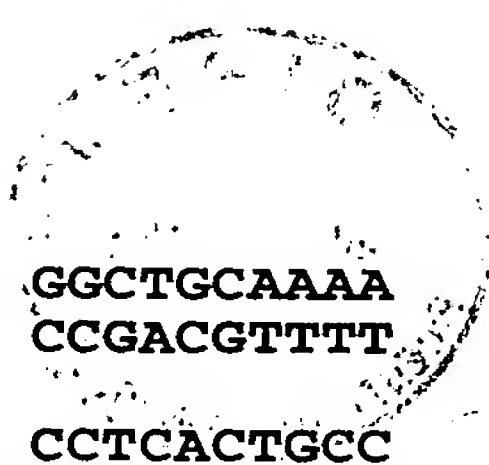
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|      | BsiWI      |             | EcoRI       |            |            |
|------|------------|-------------|-------------|------------|------------|
|      | ~~~~~      |             |             |            |            |
| 851  | AAGTTGAAAT | TAAACGTACG  | GAATTCGACT  | ATAAAGATGA | CGATGACAAA |
|      | TTCAACTTTA | ATTTGCATGC  | CTTAAGCTGA  | TATTTCTACT | GCTACTGTTT |
|      | BssHII     |             | HindIII     |            |            |
|      | ~~~~~      |             | ~~~~~       |            |            |
| 901  | GGCGCGCCGT | GGAGCCACCC  | GCAGTTTGAA  | AAATGATAAG | CTTGACCTGT |
|      | CCGCGCGGCA | CCTCGGTGGG  | CGTCAAACCTT | TTTACTATTC | GAAGTGGACA |
|      |            |             |             | OGIII3     | 100.0%     |
|      |            |             |             | =====      |            |
| 951  | GAAGTGAAAA | ATGGCGCAGA  | TTGTGCGACA  | TTTTTTTTGT | CTGCCGTTTA |
|      | CTTCACTTTT | TACCGCGTCT  | AACACGCTGT  | AAAAAAACA  | GACGGCAAAT |
|      | OGIII3     | 100.0%      |             |            |            |
|      | =====      |             |             |            |            |
| 1001 | ATTAAAGGGG | GGGGGGGGCC  | GGCCTGGGGG  | GGGGTGTACA | TGAAATTGTA |
|      | TAATTTCCCC | CCCCCCCCCG  | CCGGACCCCC  | CCCCACATGT | ACTTTAACAT |
| 1051 | AACGTTAATA | TTTTGTTAAA  | ATTCGCGTTA  | AATTTTTGTT | AAATCAGCTC |
|      | TTGCAATTAT | AAAACAATTT  | TAAGCGCAAT  | TTAAAAACAA | TTTAGTCGAG |
| 1101 | ATTTTTTAAC | CAATAGGCCG  | AAATCGGCAA  | AATCCCTTAT | AAATCAAAAG |
|      | TAAAAAATTG | GTTATCCGGC  | TTTAGCCGTT  | TTAGGGAATA | TTTAGTTTTT |
| 1151 | AATAGACCGA | GATAGGGTTG  | AGTGTGTGTC  | CAGTTTGGA  | CAAGAGTCCA |
|      | TTATCTGGCT | CTATCCCAAC  | TCACAACAAG  | GTCAAACCTT | GTTCTCAGGT |
| 1201 | CTATTAAAGA | ACGTGGACTC  | CAACGTCAAA  | GGGCGAAAAA | CCGTCTATCA |
|      | GATAATTTCT | TGCACCTGAG  | GTTGCAGTTT  | CCCGCTTTTT | GGCAGATAGT |
| 1251 | GGGCGATGGC | CCACTACGAG  | AACCATCACC  | CTAATCAAGT | TTTTTGGGGT |
|      | CCCGCTACCG | GGTGATGCTC  | TTGGTAGTGG  | GATTAGTTCA | AAAAACCCCA |
| 1301 | CGAGGTGCCG | TAAAGCACTA  | AATCGGAACC  | CTAAAGGGAG | CCCCCGATTT |
|      | GCTCCACGGC | ATTTTCGTGAT | TTAGCCTTGG  | GATTTCCCTC | GGGGGCTAAA |
| 1351 | AGAGCTTGAC | GGGGAAAGCC  | GGCGAACGTG  | GCGAGAAAGG | AAGGGAAGAA |
|      | TCTCGAACTG | CCCCTTTTCGG | CCGCTTGAC   | CGCTCTTTCC | TTCCCTTCTT |
| 1401 | AGCGAAAGGA | GCGGGCGCTA  | GGGCGCTGGC  | AAGTGTAAGC | GTCACGCTGC |
|      | TCGCTTTCCT | CGCCCGCGAT  | CCCGCGACCG  | TTACATCGC  | CAGTGCGACG |
| 1451 | GCGTAACCAC | CACACCCGCC  | GCGCTTAATG  | CGCCGCTACA | GGGCGCGTGC |
|      | CGCATTTGGT | GTGTGGGCGG  | CGCGAATTAC  | GCGGCGATGT | CCCGCGCACG |

Fig. 12 (cont.)

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|      |                          |                          |                          |                          |                          |
|------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| 1501 | TAGACTAGTG<br>ATCTGATCAC | TTTAAACCGG<br>AAATTTGGCC | ACCGGGGGGG<br>TGGCCCCCCC | GGCTTAAGTG<br>CCGAATTCAC | GGCTGCAAAA<br>CCGACGTTTT |
| 1551 | CAAAACGGCC<br>GTTTTGCCGG | TCCTGTCAGG<br>AGGACAGTCC | AAGCCGCTTT<br>TTCGGCGAAA | TATCGGGTAG<br>ATAGCCCATC | CCTCACTGCC<br>GGAGTGACGG |
| 1601 | CGCTTTCCAG<br>GCGAAAGGTC | TCGGGAAACC<br>AGCCCTTTGG | TGTCGTGCCA<br>ACAGCACGGT | GCTGCATCAG<br>CGACGTAGTC | TGAATCGGCC<br>ACTTAGCCGG |
| 1651 | AACGCGCGGG<br>TTGCGCGCCC | GAGAGGCGGT<br>CTCTCCGCCA | TTGCGTATTG<br>AACGCATAAC | GGAGCCAGGG<br>CCTCGGTCCC | TGGTTTTTCT<br>ACCAAAAAGA |
| 1701 | TTTCACCAGT<br>AAAGTGGTCA | GAGACGGGCA<br>CTCTGCCCGT | ACAGCTGATT<br>TGTCGACTAA | GCCCTTCACC<br>CGGGAAGTGG | GCCTGGCCCT<br>CGGACCGGGA |
| 1751 | GAGAGAGTTG<br>CTCTCTCAAC | CAGCAAGCGG<br>GTCGTTGCGC | TCCACGCTGG<br>AGGTGCGACC | TTTGCCCCAG<br>AAACGGGGTC | CAGGCGAAAA<br>GTCCGCTTTT |
| 1801 | TCCTGTTTGA<br>AGGACAAACT | TGGTGGTCAG<br>ACCACCAGTC | CGGCGGGATA<br>GCCGCCCTAT | TAACATGAGC<br>ATTGTACTCG | TGTCCTCGGT<br>ACAGGAGCCA |
| 1851 | ATCGTCGTAT<br>TAGCAGCATA | CCCCTACCG<br>GGGTGATGGC  | AGATGTCGCG<br>TCTACAGGCG | ACCAACGCGC<br>TGGTTGCGCG | AGCCCGGACT<br>TCGGGCCTGA |
| 1901 | CGGTAATGGC<br>GCCATTACCG | ACGCATTGCG<br>TGCGTAACGC | CCCAGCGCCA<br>GGGTCGCGGT | TCTGATCGTT<br>AGACTAGCAA | GGCAACCAGC<br>CCGTTGGTCG |
| 1951 | ATCGCAGTGG<br>TAGCGTCACC | GAACGATGCC<br>CTTGCTACGG | CTCATTCAGC<br>GAGTAAGTCG | ATTTGCATGG<br>TAAACGTACC | TTTGTGAAA<br>AAACAACTTT  |
| 2001 | ACCGGACATG<br>TGGCCTGTAC | GCACTCCAGT<br>CGTGAGGTCA | CGCCTTCCCG<br>GCGGAAGGGC | TTCCGCTATC<br>AAGGCGATAG | GGCTGAATTT<br>CCGACTTAAA |
| 2051 | GATTGCGAGT<br>CTAACGCTCA | GAGATATTTA<br>CTCTATAAAT | TGCCAGCCAG<br>ACGGTCGGTC | CCAGACGCAG<br>GGTCTGCGTC | ACGCGCCGAG<br>TGCGCGGCTC |
| 2101 | ACAGAACTTA<br>TGTCTTGAAT | ATGGGCCAGC<br>TACCCGGTCG | TAACAGCGCG<br>ATTGTCGCGC | ATTTGCTGGT<br>TAAACGACCA | GGCCCAATGC<br>CCGGGTTACG |
| 2151 | GACCAGATGC<br>CTGGTCTACG | TCCACGCCCA<br>AGGTGCGGGT | GTCGCGTACC<br>CAGCGCATGG | GTCCTCATGG<br>CAGGAGTACC | GAGAAAATAA<br>CTCTTTTATT |
| 2201 | TACTGTTGAT<br>ATGACAATA  | GGGTGTCTGG<br>CCCACAGACC | TCAGAGACAT<br>AGTCTCTGTA | CAAGAAATAA<br>GTTCTTTATT | CGCCGGAACA<br>GCGGCCTTGT |
| 2251 | TTAGTGCAGG<br>AATCACGTCC | CAGCTTCCAC<br>GTCGAAGGTG | AGCAATAGCA<br>TCGTTATCGT | TCCTGGTCAT<br>AGGACCAGTA | CCAGCGGATA<br>GGTCGCCTAT |

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Fig. 12 (cont.)



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2301	GTTAATAATC CAATTATTAG	AGCCCACTGA TCGGGTGACT	CACGTTGCGC GTGCAACGCG	GAGAAGATTG CTCTTCTAAC	TGCACCGCCG ACGTGGCGGC
2351	CTTTACAGGC GAAATGTCCG	TTCGACGCCG AAGCTGCGGC	CTTCGTTCTA GAAGCAAGAT	CCATCGACAC GGTAGCTGTG	GACCACGCTG CTGGTGCGAC
2401	GCACCCAGTT CGTGGGTCAA	GATCGGCGCG CTAGCCGCGC	AGATTTAATC TCTAAATTAG	GCCGCGACAA CGGCGCTGTT	TTTGCGACGG AAACGCTGCC
2451	CGCGTGCAGG GCGCACGTCC	GCCAGACTGG CGGTCTGACC	AGGTGGCAAC TCCACCGTTG	GCCAATCAGC CGGTTAGTCG	AACGACTGTT TTGCTGACAA
2501	TGCCCCGCCAG ACGGGCGGTC	TTGTTGTGCC AACAACACGG	ACGCGGTTAG TGCGCCAATC	GAATGTAATT CTTACATTAA	CAGCTCCGCC GTCGAGGCGG
2551	ATCGCCGCTT TAGCGGCGAA	CCACTTTTTT GGTGAAAAAG	CCGCGTTTTT GGCGCAAAAG	GCAGAAACGT CGTCTTTGCA	GGCTGGCCTG CCGACCGGAC
2601	G TTCACCACG CAAGTGGTGC	CGGGAAACGG GCCCTTTGCC	TCTGATAAGA AGACTATTCT	GACACCGGCA CTGTGGCCGT	TACTCTGCGA ATGAGACGCT
2651	CATCGTATAA GTAGCATATT	CGTTACTGGT GCAATGACCA	TTCACATTCA AAGTGTAAGT	CCACCCTGAA GGTGGGACTT	TTGACTCTCT AACTGAGAGA
2701	TCCGGGCGCT AGGCCCGCGA	ATCATGCCAT TAGTACGGTA	ACCGCGAAAG TGGCGCTTTC	GTTTTGCGCC CAAAACGCGG	ATTCGATGCT TAAGCTACGA
2751	AGCCATGTGA TCGGTACACT	GCAAAAGGCC CGTTTTCCGG	AGCAAAAGGC TCGTTTTCCG	CAGGAACCGT GTCCTTGGCA	AAAAAGGCCG TTTTTCCGGC
2801	CGTTGCTGGC GCAACGACCG	GTTTTTCCAT CAAAAAGGTA	AGGCTCCGCC TCCGAGGCGG	CCCCTGACGA GGGGACTGCT	GCATCACAAA CGTAGTGTTT
2851	AATCGACGCT TTAGCTGCGA	CAAGTCAGAG GTTCAGTCTC	GTGGCGAAAC CACCGCTTTG	CCGACAGGAC GGCTGTCCTG	TATAAAGATA ATATTTCTAT
2901	CCAGGCGTTT GGTCCGCAAA	CCCCCTGGAA GGGGGACCTT	GCTCCCTCGT CGAGGGAGCA	GCGCTCTCCT CGCGAGAGGA	GTTCCGACCC CAAGGCTGGG
2951	TGCCGCTTAC ACGGCGAATG	CGGATACCTG GCCTATGGAC	TCCGCCTTTC AGGCGGAAAG	TCCCTTCGGG AGGGAAGCCC	AAGCGTGGCG TTCGCACCGC
3001	CTTTCTCATA GAAAGAGTAT	GCTCACGCTG CGAGTGCGAC	TAGGTATCTC ATCCATAGAG	AGTTCGGTGT TCAAGCCACA	AGGTCGTTCT TCCAGCAAGC

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|      |                          |                          |                          |                          |                          |
|------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| 3051 | CTCCAAGCTG<br>GAGGTTGAC  | GGCTGTGTGC<br>CCGACACACG | ACGAACCCCC<br>TGCTTGGGGG | CGTTCAGCCC<br>GCAAGTCGGG | GACCGCTGCG<br>CTGGCGACGC |
| 3101 | CCTTATCCGG<br>GGAATAGGCC | TAACTATCGT<br>ATTGATAGCA | CTTGAGTCCA<br>GAATCAGGT  | ACCCGGTAAG<br>TGGGCCATTC | ACACGACTTA<br>TGTGCTGAAT |

Fig. 12 (cont.)



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|      |                          |                          |                           |                          |                           |
|------|--------------------------|--------------------------|---------------------------|--------------------------|---------------------------|
| 3151 | TCGCCACTGG<br>AGCGGTGACC | CAGCAGCCAC<br>GTCGTCGGTG | TGGTAACAGG<br>ACCATTTGTCC | ATTAGCAGAG<br>TAATCGTCTC | CGAGGTATGT<br>GCTCCATACA  |
| 3201 | AGGCGGTGCT<br>TCCGCCACGA | ACAGAGTTCT<br>TGTCTCAAGA | TGAAGTGGTG<br>ACTTCACCAC  | GCCTAACTAC<br>CGGATTGATG | GGCTACACTA<br>CCGATGTGAT  |
| 3251 | GAAGAACAGT<br>CTTCTTGTCA | ATTTGGTATC<br>TAAACCATAG | TGCGCTCTGC<br>ACGCGAGACG  | TGTAGCCAGT<br>ACATCGGTCA | TACCTTCGGA<br>ATGGAAGCCT  |
| 3301 | AAAAGAGTTG<br>TTTTCTCAAC | GTAGCTCTTG<br>CATCGAGAAC | ATCCGGCAAA<br>TAGGCCGTTT  | CAAACCACCG<br>GTTTGGTGGC | CTGGTAGCGG<br>GACCATCGCC  |
| 3351 | TGGTTTTTTT<br>ACCAAAAAAA | GTTTGCAAGC<br>CAAACGTTTC | AGCAGATTAC<br>TCGTCTAATG  | GCGCAGAAAA<br>CGCGTCTTTT | AAAGGATCTC<br>TTTCCTAGAG  |
| 3401 | AAGAAGATCC<br>TTCTTCTAGG | TTTGATCTTT<br>AAACTAGAAA | TCTACGGGGT<br>AGATGCCCCA  | CTGACGCTCA<br>GACTGCGAGT | GTGGAACGAA<br>CACCTTGCTT  |
| 3451 | AACTCACGTT<br>TTGAGTGCAA | AAGGGATTTT<br>TTCCCTAAAA | GGTCAGATCT<br>CCAGTCTAGA  | AGCACCAGGC<br>TCGTGGTCCG | GTTTAAGGGC<br>CAAATTCCCG  |
| 3501 | ACCAATAACT<br>TGGTTATTGA | GCCTTAAAAA<br>CGGAATTTTT | AATTACGCCC<br>TTAATGCGGG  | CGCCCTGCCA<br>GCGGGACGGT | CTCATCGCAG<br>GAGTAGCGTC  |
| 3551 | TACTGTTGTA<br>ATGACAACAT | ATTCATTAAG<br>TAAGTAATTC | CATTCTGCCG<br>GTAAGACGGC  | ACATGGAAGC<br>TGTACCTTCG | CATCACAAAC<br>GTAGTGTTTG  |
| 3601 | GGCATGATGA<br>CCGTACTACT | ACCTGAATCG<br>TGGACTTAGC | CCAGCGGCAT<br>GGTCGCCGTA  | CAGCACCTTG<br>GTCGTGGAAC | TCGCCTTGCG<br>AGCGGAACGC  |
| 3651 | TATAATATTT<br>ATATTATAAA | GCCCATAGTG<br>CGGGTATCAC | AAAACGGGGG<br>TTTTGCCCCC  | CGAAGAAGTT<br>GCTTCTTCAA | GTCCATATTG<br>CAGGTATAAC  |
| 3701 | GCTACGTTTA<br>CGATGCAAAT | AATCAAAACT<br>TTAGTTTTGA | GGTGAAACTC<br>CCACTTTGAG  | ACCCAGGGAT<br>TGGGTCCCTA | TGGCTGAGAC<br>ACCGACTCTG  |
| 3751 | GAAAAACATA<br>CTTTTTGTAT | TTCTCAATAA<br>AAGAGTTATT | ACCCTTTAGG<br>TGGGAAATCC  | GAAATAGGCC<br>CTTTATCCGG | AGGTTTTTCAC<br>TCCAAAAGTG |
| 3801 | CGTAACACGC<br>GCATTGTGCG | CACATCTTGC<br>GTGTAGAACG | GAATATATGT<br>CTTATATACA  | GTAGAAACTG<br>CATCTTTGAC | CCGGAAATCG<br>GGCCTTTAGC  |
| 3851 | TCGTGGTATT<br>AGCACCATAA | CACTCCAGAG<br>GTGAGGTCTC | CGATGAAAAC<br>GCTACTTTTG  | GTTTCAGTTT<br>CAAAGTCAAA | GCTCATGGAA<br>CGAGTACCTT  |
| 3901 | AACGGTGTA<br>TTGCCACATT  | CAAGGGTGAA<br>GTTCCCACTT | CACTATCCCA<br>GTGATAGGGT  | TATCACCAGC<br>ATAGTGGTCG | TCACCGTCTT<br>AGTGGCAGAA  |
| 3951 | TCATTGCCAT<br>AGTAACGGTA | ACGGAACTCC<br>TGCCTTGAGG | GGGTGAGCAT<br>CCCACTCGTA  | TCATCAGGCG<br>AGTAGTCCGC | GGCAAGAATG<br>CCGTTCTTAC  |

Fig. 12 (cont.)

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4001 TGAATAAAGG CCGGATAAAA CTTGTGCTTA TTTTCTTTA CGGTCTTTAA  
 ACTTATTTCC GGCCTATTTT GAACACGAAT AAAAAGAAAT GCCAGAAATT  
 4051 AAAGGCCGTA ATATCCAGCT GAACGGTCTG GTTATAGGTA CATTGAGCAA  
 TTCCGGCAT TATAGGTCGA CTTGCCAGAC CAATATCCAT GTAACTCGTT  
 4101 CTGACTGAAA TGCCTCAAAA TGTTCCTTAC GATGCCATTG GGATATATCA  
 GACTGACTTT ACGGAGTTTT ACAAGAAATG CTACGGTAAC CCTATATAGT  
 4151 ACGGTGGTAT ATCCAGTGAT TTTTTTCTCC ATTTTAGCTT CCTTAGCTCC  
 TGCCACCATA TAGGTCATA AAAAAGAGG TAAATCGAA GGAATCGAGG  
 4201 TGAAAATCTC GATAACTCAA AAAATACGCC CGGTAGTGAT CTTATTTTCAT  
 ACTTTTAGAG CTATTGAGTT TTTTATGCGG GCCATCACTA GAATAAAGTA  
 4251 TATGGTGAAA GTTGGAACCT CACCCGACGT CTAATGTGAG TTAGCTCACT  
 ATACCACTTT CAACCTTGGA GTGGGCTGCA GATTACACTC AATCGAGTGA  
 4301 CATTAGGCAC CCCAGGCTTT ACACTTTATG CTTCCGGCTC GTATGTTGTG  
 GTAATCCGTG GGGTCCGAAA TGTGAAATAC GAAGGCCGAG CATAACAAC  
 M13 Reverse primer 100.0%  
 =====  
 4351 TGGAATTGTG AGCGGATAAC AATTTACAC AGGAAACAGC TATGACCATG  
 ACCTTAACAC TCGCCTATTG TTAAAGTGTG TCCTTTGTG AACTGGTAC  
 4401 ATTACGAATT  
 TAATGCTTAA

Fig. 12 (cont.)

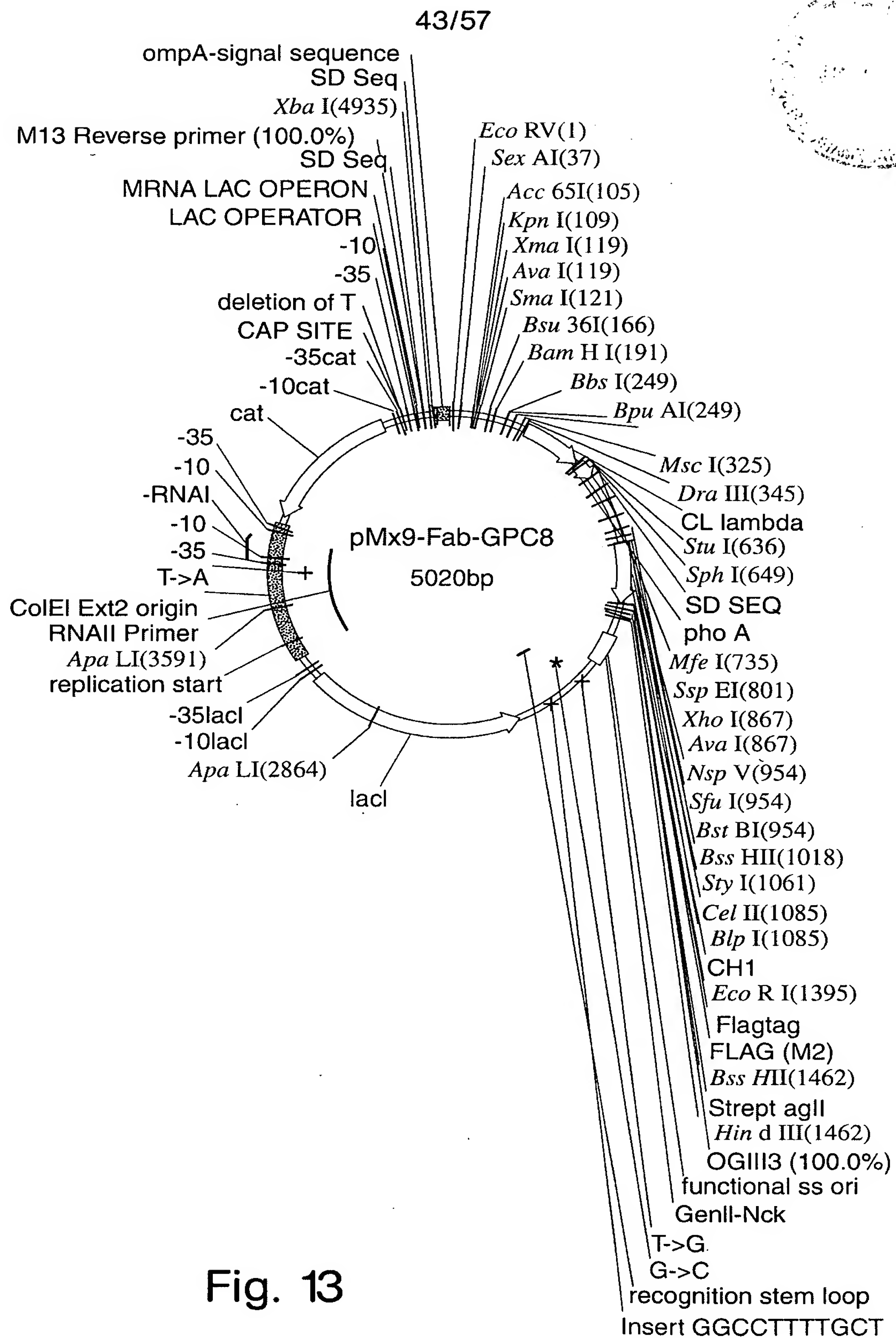


Fig. 13



ATGAGGG  
TACTCCC

**B1pI**

Fig. 13 (cont.)

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|      |                          | StyI                     |                          |                           | ~~~~~<br>CelII<br>~~~~~  |  |
|------|--------------------------|--------------------------|--------------------------|---------------------------|--------------------------|--|
| 1051 | TTATTGGGGC<br>AATAACCCCG | CAAGGCACCC<br>GTTCCGTGGG | TGGTGACGGT<br>ACCACTGCCA | TAGCTCAGCG<br>ATCGAGTCGC  | TCGACCAAAG<br>AGCTGGTTTC |  |
| 1101 | GTCCAAGCGT<br>CAGGTTCGCA | GTTTCCGCTG<br>CAAAGGCGAC | GCTCCGAGCA<br>CGAGGCTCGT | GCAAAAGCAC<br>CGTTTTTCGTG | CAGCGGCGGC<br>GTCGCCGCCG |  |
| 1151 | ACGGCTGCCC<br>TGCCGACGGG | TGGGCTGCCT<br>ACCCGACGGA | GGTTAAAGAT<br>CCAATTTCTA | TATTTCCCGG<br>ATAAAGGGCC  | AACCAGTCAC<br>TTGGTCAGTG |  |
| 1201 | CGTGAGCTGG<br>GCACTCGACC | AACAGCGGGG<br>TTGTCGCCCC | CGCTGACCAG<br>GCGACTGGTC | CGGCGTG CAT<br>GCCGCACGTA | ACCTTTCCGG<br>TGGAAAGGCC |  |
| 1251 | CGGTGCTGCA<br>GCCACGACGT | AAGCAGCGGC<br>TTCGTCGCCG | CTGTATAGCC<br>GACATATCGG | TGAGCAGCGT<br>ACTCGTCGCA  | TGTGACCGTG<br>ACACTGGCAC |  |
| 1301 | CCGAGCAGCA<br>GGCTCGTCGT | GCTTAGGCAC<br>CGAATCCGTG | TCAGACCTAT<br>AGTCTGGATA | ATTTGCAACG<br>TAAACGTTGC  | TGAACCATAA<br>ACTTGGTATT |  |
|      |                          |                          |                          |                           | EcoRI<br>~~~~~           |  |
| 1351 | ACCGAGCAAC<br>TGGCTCGTTG | ACCAAAGTGG<br>TGGTTTCACC | ATAAAAAAGT<br>TATTTTTTCA | GGAACCGAAA<br>CCTTGGCTTT  | AGCGAATTCG<br>TCGCTTAAGC |  |
|      |                          |                          | BssHII<br>~~~~~          |                           |                          |  |
| 1401 | ACTATAAAGA<br>TGATATTTCT | TGACGATGAC<br>ACTGCTACTG | AAAGGCGCGC<br>TTTCCGCGCG | CGTGGAGCCA<br>GCACCTCGGT  | CCCGCAGTTT<br>GGGCGTCAAA |  |
|      |                          | HindIII<br>~~~~~         |                          |                           |                          |  |
| 1451 | GAAAAATGAT<br>CTTTTTACTA | AAGCTTGACC<br>TTCGAACTGG | TGTGAAGTGA<br>ACACTTCACT | AAAATGGCGC<br>TTTTACCGCG  | AGATTGTGCG<br>TCTAACACGC |  |
|      |                          |                          | OGIII3 100.0%            |                           |                          |  |
|      |                          |                          | =====                    |                           |                          |  |
| 1501 | ACATTTTTTT<br>TGTAACAAAA | TGTCTGCCGT<br>ACAGACGGCA | TTAATTAAAG<br>AATTAATTTT | GGGGGGGGGG<br>CCCCCCCC    | GCCGGCCTGG<br>CGGCCGGACC |  |
| 1551 | GGGGGGGTGT<br>CCCCCCCACA | ACATGAAATT<br>TGTACTTTAA | GTAAACGTTA<br>CATTTGCAAT | ATATTTTGTT<br>TATAAAACAA  | AAAATTCGCG<br>TTTAAAGCGC |  |
| 1601 | TTAAATTTTT<br>AATTTAAAAA | GTAAATCAG<br>CAATTTAGTC  | CTCATTTTTT<br>GAGTAAAAAA | AACCAATAGG<br>TTGGTTATCC  | CCGAAATCGG<br>GGCTTTAGCC |  |
| 1651 | CAAAATCCCT<br>GTTTTAGGGA | TATAAATCAA<br>ATATTTAGTT | AAGAATAGAC<br>TTCTTATCTG | CGAGATAGGG<br>GCTCTATCCC  | TTGAGTGTTG<br>AACTCACAAC |  |
| 1701 | TTCCAGTTTG<br>AAGGTCAAAC | GAACAAGAGT<br>CTTGTTCTCA | CCACTATTAA<br>GGTGATAATT | AGAACGTGGA<br>TCTTGACACT  | CTCCAACGTC<br>GAGGTTGCAG |  |

Fig. 13 (cont.)



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|      |                          |                           |                          |                          |                          |
|------|--------------------------|---------------------------|--------------------------|--------------------------|--------------------------|
| 1751 | AAAGGGCGAA<br>TTTCCCGCTT | AAACCGTCTA<br>TTTGGCAGAT  | TCAGGGCGAT<br>AGTCCCGCTA | GGCCCACTAC<br>CCGGGTGATG | GAGAACCATC<br>CTCTTGGTAG |
| 1801 | ACCCTAATCA<br>TGGGATTAGT | AGTTTTTTTGG<br>TCAAAAAACC | GGTCGAGGTG<br>CCAGCTCCAC | CCGTAAAGCA<br>GGCATTTCGT | CTAAATCGGA<br>GATTTAGCCT |
| 1851 | ACCCTAAAGG<br>TGGGATTTCC | GAGCCCCCGA<br>CTCGGGGGCT  | TTTAGAGCTT<br>AAATCTCGAA | GACGGGGGAA<br>CTGCCCTTT  | GCCGGCGAAC<br>CGGCCGCTTG |
| 1901 | GTGGCGAGAA<br>CACCGCTCTT | AGGAAGGGAA<br>TCCTTCCCTT  | GAAAGCGAAA<br>CTTTCGCTTT | GGAGCGGGCG<br>CCTCGCCCGC | CTAGGGCGCT<br>GATCCCGCGA |
| 1951 | GGCAAGTGTA<br>CCGTTCACAT | GCGGTCACGC<br>CGCCAGTGCG  | TGCGCGTAAC<br>ACGCGCATTG | CACCACACCC<br>GTGGTGTGGG | GCCGCGCTTA<br>CGGCGCGAAT |
| 2001 | ATGCGCCGCT<br>TACGCGGCGA | ACAGGGCGCG<br>TGTCCCGCGC  | TGCTAGACTA<br>ACGATCTGAT | GTGTTTAAAC<br>CACAAATTTG | CGGACCGGGG<br>GCCTGGCCCC |
| 2051 | GGGGGCTTAA<br>CCCCCGAATT | GTGGGCTGCA<br>CACCCGACGT  | AAACAAAACG<br>TTTGTTTTGC | GCCTCCTGTC<br>CGGAGGACAG | AGGAAGCCGC<br>TCCTTCGGCG |
| 2101 | TTTTATCGGG<br>AAAATAGCCC | TAGCCTCACT<br>ATCGGAGTGA  | GCCCGCTTTC<br>CGGGCGAAAG | CAGTCGGGAA<br>GTCAGCCCTT | ACCTGTCGTG<br>TGGACAGCAC |
| 2151 | CCAGCTGCAT<br>GGTCGACGTA | CAGTGAATCG<br>GTCACTTAGC  | GCCAACGCGC<br>CGGTTGCGCG | GGGGAGAGGC<br>CCCCTCTCCG | GGTTTGCGTA<br>CCAAACGCAT |
| 2201 | TTGGGAGCCA<br>AACCCTCGGT | GGGTGGTTTT<br>CCCACCAAAA  | TCTTTTCACC<br>AGAAAAGTGG | AGTGAGACGG<br>TCACTCTGCC | GCAACAGCTG<br>CGTTGTCGAC |
| 2251 | ATTGCCCTTC<br>TAACGGGAAG | ACCGCCTGGC<br>TGGCGGACCG  | CCTGAGAGAG<br>GGACTCTCTC | TTGCAGCAAG<br>AACGTCGTTC | CGGTCCACGC<br>GCCAGGTGCG |
| 2301 | TGGTTTGCCC<br>ACCAAACGGG | CAGCAGGCGA<br>GTCGTCCGCT  | AAATCCTGTT<br>TTTAGGACAA | TGATGGTGGT<br>ACTACCACCA | CAGCGGCGGG<br>GTCGCCGCCC |
| 2351 | ATATAACATG<br>TATATTGTAC | AGCTGTCCTC<br>TCGACAGGAG  | GGTATCGTCG<br>CCATAGCAGC | TATCCCCTA<br>ATAGGGTGAT  | CCGAGATGTC<br>GGCTCTACAG |
| 2401 | CGCACCAACG<br>GCGTGGTTGC | CGCAGCCCGG<br>GCGTCGGGCC  | ACTCGGTAAT<br>TGAGCCATTA | GGCACGCATT<br>CCGTGCGTAA | GCGCCCAGCG<br>CGCGGGTCGC |
| 2451 | CCATCTGATC<br>GGTAGACTAG | GTTGGCAACC<br>CAACCGTTGG  | AGCATCGCAG<br>TCGTAGCGTC | TGGGAACGAT<br>ACCCTTGCTA | GCCCTCATTC<br>CGGGAGTAAG |
| 2501 | AGCATTTGCA<br>TCGTAAACGT | TGGTTTGTTG<br>ACCAAACAAC  | AAAACCGGAC<br>TTTTGGCCTG | ATGGCACTCC<br>TACCGTGAGG | AGTCGCCTTC<br>TCAGCGGAAG |
| 2551 | CCGTTCCGCT<br>GGCAAGGCGA | ATCGGCTGAA<br>TAGCCGACTT  | TTTGATTGCG<br>AAACTAACGC | AGTGAGATAT<br>TCACTCTATA | TTATGCCAGC<br>AATACGGTCG |

Fig. 13 (cont.)

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|                |                          |                          |                          |                          |                          |
|----------------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| 2601           | CAGCCAGACG<br>GTCGGTCTGC | CAGACGCGCC<br>GTCTGCGCGG | GAGACAGAAC<br>CTCTGTCTTG | TTAATGGGEC<br>AATTACCCGG | AGCTAACAGC<br>TCGATTGTCT |
| 2651           | GCGATTTGCT<br>CGCTAAACGA | GGTGGCCCAA<br>CCACCGGGTT | TGCGACCAGA<br>ACGCTGGTCT | TGCTCCACGC<br>ACGAGGTGCG | CCAGTCGCGT<br>GGTCAGCGCA |
| 2701           | ACCGTCCTCA<br>TGGCAGGAGT | TGGGAGAAAA<br>ACCCTCTTTT | TAATACTGTT<br>ATTATGACAA | GATGGGTGTC<br>CTACCCACAG | TGGTCAGAGA<br>ACCAGTCTCT |
| 2751           | CATCAAGAAA<br>GTAGTTCTTT | TAACGCCGGA<br>ATTGCGGCCT | ACATTAGTGC<br>TGTAATCACG | AGGCAGCTTC<br>TCCGTCGAAG | CACAGCAATA<br>GTGTCGTTAT |
| 2801           | GCATCCTGGT<br>CGTAGGACCA | CATCCAGCGG<br>GTAGGTCGCC | ATAGTTAATA<br>TATCAATTAT | ATCAGCCCAC<br>TAGTCGGGTG | TGACACGTTG<br>ACTGTGCAAC |
| ApaLI<br>~~~~~ |                          |                          |                          |                          |                          |
| 2851           | CGCGAGAAGA<br>GCGCTCTTCT | TTGTGCACCG<br>AACACGTGGC | CCGCTTTACA<br>GGCGAAATGT | GGCTTCGACG<br>CCGAAGCTGC | CCGCTTCGTT<br>GGCGAAGCAA |
| 2901           | CTACCATCGA<br>GATGGTAGCT | CACGACCACG<br>GTGCTGGTGC | CTGGCACCCA<br>GACCGTGGGT | GTTGATCGGC<br>CAACTAGCCG | GCGAGATTTA<br>CGCTCTAAAT |
| 2951           | ATCGCCGCGA<br>TAGCGGCGCT | CAATTTGCGA<br>GTTAAACGCT | CGGCGCGTGC<br>GCCGCGCACG | AGGGCCAGAC<br>TCCCGGTCTG | TGGAGGTGGC<br>ACCTCCACCG |
| 3001           | AACGCCAATC<br>TTGCGGTTAG | AGCAACGACT<br>TCGTTGCTGA | GTTTGCCCGC<br>CAAACGGGCG | CAGTTGTTGT<br>GTCAACAACA | GCCACGCGGT<br>CGGTGCGCCA |
| 3051           | TAGGAATGTA<br>ATCCTTACAT | ATTCAGCTCC<br>TAAGTCGAGG | GCCATCGCCG<br>CGGTAGCGGC | CTTCCACTTT<br>GAAGGTGAAA | TTCCCGCGTT<br>AAGGGCGCAA |
| 3101           | TTCGCAGAAA<br>AAGCGTCTTT | CGTGGCTGGC<br>GCACCGACCG | CTGGTTCACC<br>GACCAAGTGG | ACGCGGGAAA<br>TGCGCCCTTT | CGGTCTGATA<br>GCCAGACTAT |
| 3151           | AGAGACACCG<br>TCTCTGTGGC | GCATACTCTG<br>CGTATGAGAC | CGACATCGTA<br>GCTGTAGCAT | TAACGTTACT<br>ATTGCAATGA | GGTTTCACAT<br>CCAAAGTGTA |
| 3201           | TCACCACCCT<br>AGTGGTGGGA | GAATTGACTC<br>CTTAAGTGAG | TCTTCCGGGC<br>AGAAGGCCCG | GCTATCATGC<br>CGATAGTACG | CATACGCGA<br>GTATGGCGCT  |
| 3251           | AAGGTTTTGC<br>TTCCAAAACG | GCCATTCGAT<br>CGGTAAGCTA | GCTAGCCATG<br>CGATCGGTAC | TGAGCAAAAG<br>ACTCGTTTTT | GCCAGCAAAA<br>CGGTGTTTTT |
| 3301           | GGCCAGGAAC<br>CCGGTCCTTG | CGTAAAAAGG<br>GCATTTTTTC | CCGCGTTGCT<br>GGCGCAACGA | GGCGTTTTTC<br>CCGCAAAAAG | CATAGGCTCC<br>GTATCCGAGG |
| 3351           | GCCCCCTGA<br>CGGGGGGACT  | CGAGCATCAC<br>GCTCGTAGTG | AAAAATCGAC<br>TTTTTAGCTG | GCTCAAGTCA<br>CGAGTTCAGT | GAGGTGGCGA<br>CTCCACCGCT |
| 3401           | AACCCGACAG               | GACTATAAAG               | ATACCAGGCG               | TTTCCCCCTG               | GAAGCTCCCT               |

Fig. 13 (cont.)



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|      |                          |                          |                           |                          |                           |
|------|--------------------------|--------------------------|---------------------------|--------------------------|---------------------------|
|      | TTGGGCTGTC               | CTGATATTTTC              | TATGGTCCGC                | AAAGGGGGAC               | CTTCGAGGGA                |
| 3451 | CGTGCGCTCT<br>GCACGCGAGA | CCTGTTCCGA<br>GGACAAGGCT | CCCTGCCGCT<br>GGGACGGCGA  | TACCGGATAC<br>ATGGCCTATG | CTGTCCGCCT<br>GACAGGCGGA  |
| 3501 | TTCTCCCTTC<br>AAGAGGGAAG | GGGAAGCGTG<br>CCCTTCGCAC | GCGCTTTCTC<br>CGCGAAAGAG  | ATAGCTCACG<br>TATCGAGTGC | CTGTAGGTAT<br>GACATCCATA  |
|      |                          |                          |                           | ApaLI<br>~~~~~           |                           |
| 3551 | CTCAGTTCGG<br>GAGTCAAGCC | TGTAGGTCGT<br>ACATCCAGCA | TCGCTCCAAG<br>AGCGAGGTTC  | CTGGGCTGTG<br>GACCCGACAC | TGCACGAACC<br>ACGTGCTTGG  |
| 3601 | CCCCGTTCAG<br>GGGGCAAGTC | CCCGACCGCT<br>GGGCTGGCGA | GCGCCTTATC<br>CGCGGAATAG  | CGGTAACAT<br>GCCATTGATA  | CGTCTTGAGT<br>GCAGAACTCA  |
| 3651 | CCAACCCGGT<br>GGTTGGGCCA | AAGACACGAC<br>TTCTGTGCTG | TTATCGCCAC<br>AATAGCGGTG  | TGGCAGCAGC<br>ACCGTCGTCG | CACTGGTAAC<br>GTGACCATTG  |
| 3701 | AGGATTAGCA<br>TCCTAATCGT | GAGCGAGGTA<br>CTCGCTCCAT | TGTAGGCGGT<br>ACATCCGCCA  | GCTACAGAGT<br>CGATGTCTCA | TCTTGAAGTG<br>AGAACTTCAC  |
| 3751 | GTGGCCTAAC<br>CACCGGATTG | TACGGCTACA<br>ATGCCGATGT | CTAGAAGAAC<br>GATCTTCTTG  | AGTATTTGGT<br>TCATAAACCA | ATCTGCGCTC<br>TAGACGCGAG  |
| 3801 | TGCTGTAGCC<br>ACGACATCGG | AGTTACCTTC<br>TCAATGGAAG | GGAAAAAGAG<br>CCTTTTTTCTC | TTGGTAGCTC<br>AACCATCGAG | TTGATCCGGC<br>AACTAGGCCG  |
| 3851 | AAACAAACCA<br>TTTGTTTGGT | CCGCTGGTAG<br>GGCGACCATC | CGGTGGTTTT<br>GCCACCAAAA  | TTTGTTTGCA<br>AAACAAACGT | AGCAGCAGAT<br>TCGTCTGTCTA |
| 3901 | TACGCGCAGA<br>ATGCGCGTCT | AAAAAAGGAT<br>TTTTTTCCTA | CTCAAGAAGA<br>GAGTTCTTCT  | TCCTTTGATC<br>AGGAAACTAG | TTTTCTACGG<br>AAAAGATGCC  |
| 3951 | GGTCTGACGC<br>CCAGACTGCG | TCAGTGGAAC<br>AGTCACCTTG | GAAAACCTCAC<br>CTTTTGAGTG | GTTAAGGGAT<br>CAATTCCCTA | TTTGGTCAGA<br>AAACCAGTCT  |
| 4001 | TCTAGCACCA<br>AGATCGTGGT | GGCGTTTAAG<br>CCGCAAATTC | GGCACCAATA<br>CCGTGGTTAT  | ACTGCCTTAA<br>TGACGGAATT | AAAAATTACG<br>TTTTTAATGC  |
| 4051 | CCCCGCCCTG<br>GGGGCGGGAC | CCACTCATCG<br>GGTGAGTAGC | CAGTACTGTT<br>GTCATGACAA  | GTAATTCATT<br>CATTAAGTAA | AAGCATTCTG<br>TTCGTAAGAC  |
| 4101 | CCGACATGGA<br>GGCTGTACCT | AGCCATCACA<br>TCGGTAGTGT | AACGGCATGA<br>TTGCCGTACT  | TGAACCTGAA<br>ACTTGGACTT | TCGCCAGCGG<br>AGCGGTGCGC  |
| 4151 | CATCAGCAC<br>GTAGTCGTGG  | TTGTCGCCTT<br>AACAGCGGAA | GCGTATAATA<br>CGCATATTAT  | TTTGCCCAT<br>AAACGGGTAT  | GTGAAAACGG<br>CACTTTTGCC  |
| 4201 | GGGCGAAGAA<br>CCCGCTTCTT | GTTGTCCATA<br>CAACAGGTAT | TTGGCTACGT<br>AACCGATGCA  | TTAAATCAAA<br>AATTTAGTTT | ACTGGTGAAA<br>TGACCACTTT  |

Fig. 13 (cont.)

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|      |                           |            |            |            |            |
|------|---------------------------|------------|------------|------------|------------|
| 4251 | CTCACCCAGG                | GATTGGCTGA | GACGAAAAAC | ATATTCTCAA | TAAACCCTTT |
|      | GAGTGGGTCC                | CTAACCGACT | CTGCTTTTTG | TATAAGAGTT | ATTTGGGAAA |
| 4301 | AGGGAAATAG                | GCCAGGTTTT | CACCGTAACA | CGCCACATCT | TGCGAATATA |
|      | TCCCTTTATC                | CGGTCCAAAA | GTGGCATTGT | GCGGTGTAGA | ACGCTTATAT |
| 4351 | TGTGTAGAAA                | CTGCCGGA   | TCGTCGTGGT | ATTCACCTCA | GAGCGATGAA |
|      | ACACATCTTT                | GACGGCCTTT | AGCAGCACCA | TAAGTGAGGT | CTCGCTACTT |
| 4401 | AACGTTTCAG                | TTTGCTCATG | GAAAACGGTG | TAACAAGGGT | GAACACTATC |
|      | TTGCAAAGTC                | AAACGAGTAC | CTTTTGCCAC | ATTGTTCCCA | CTTGTGATAG |
| 4451 | CCATATCACC                | AGCTCACCGT | CTTTCATTGC | CATACGGAAC | TCCGGGTGAG |
|      | GGTATAGTGG                | TCGAGTGGCA | GAAAGTAACG | GTATGCCTTG | AGGCCCACTC |
| 4501 | CATTCATCAG                | GCGGGCAAGA | ATGTGAATAA | AGGCCGGATA | AAACTTGTGC |
|      | GTAAGTAGTC                | CGCCCGTTCT | TACACTTATT | TCCGGCCTAT | TTTGAACACG |
| 4551 | TTATTTTTCT                | TTACGGTCTT | TAAAAAGGCC | GTAATATCCA | GCTGAACGGT |
|      | AATAAAAAGA                | AATGCCAGAA | ATTTTCCGG  | CATTATAGGT | CGACTTGCCA |
| 4601 | CTGGTTATAG                | GTACATTGAG | CAACTGACTG | AAATGCCTCA | AAATGTTCTT |
|      | GACCAATATC                | CATGTAATC  | GTTGACTGAC | TTTACGGAGT | TTTACAAGAA |
| 4651 | TACGATGCCA                | TTGGGATATA | TCAACGGTGG | TATATCCAGT | GATTTTTTTC |
|      | ATGCTACGGT                | AACCCTATAT | AGTTGCCACC | ATATAGGTCA | CTAAAAAAG  |
| 4701 | TCCATTTTAG                | CTTCCTTAGC | TCCTGAAAAT | CTCGATAACT | CAAAAAATAC |
|      | AGGTAAAATC                | GAAGGAATCG | AGGACTTTTA | GAGCTATTGA | GTTTTTTATG |
| 4751 | GCCCGGTAGT                | GATCTTATTT | CATTATGGTG | AAAGTTGGAA | CCTCACCCGA |
|      | CGGGCCATCA                | CTAGAATAAA | GTAATACCAC | TTTCAACCTT | GGAGTGGGCT |
| 4801 | CGTCTAATGT                | GAGTTAGCTC | ACTCATTAGG | CACCCCAGGC | TTTACACTTT |
|      | GCAGATTACA                | CTCAATCGAG | TGAGTAATCC | GTGGGGTCCG | AAATGTGAAA |
| 4851 | ATGCTTCCGG                | CTCGTATGTT | GTGTGGAATT | GTGAGCGGAT | AACAATTTCA |
|      | TACGAAGGCC                | GAGCATACAA | CACACCTTAA | CACTCGCCTA | TTGTTAAAGT |
|      | M13 Reverse primer 100.0% |            |            | XbaI       |            |
|      | =====                     |            |            | ~~~~~      |            |
| 4901 | CACAGGAAAC                | AGCTATGACC | ATGATTACGA | ATTTCTAGAT | AACGAGGGCA |
|      | GTGTCCTTTG                | TCGATACTGG | TACTAATGCT | TAAAGATCTA | TTGCTCCCGT |
| 4951 | AAAAATGAAA                | AAGACAGCTA | TCGCGATTGC | AGTGGCACTG | GCTGGTTTCG |
|      | TTTTTACTTT                | TTCTGTCGAT | AGCGCTAACG | TCACCGTGAC | CGACCAAAGC |
|      | EcoRV                     |            |            |            |            |
|      | ~~~                       |            |            |            |            |
| 5001 | CTACCGTAGC                | GCAGGCCGAT |            |            |            |
|      | GATGGCATCG                | CGTCCGGCTA |            |            |            |

Fig. 13 (cont.)

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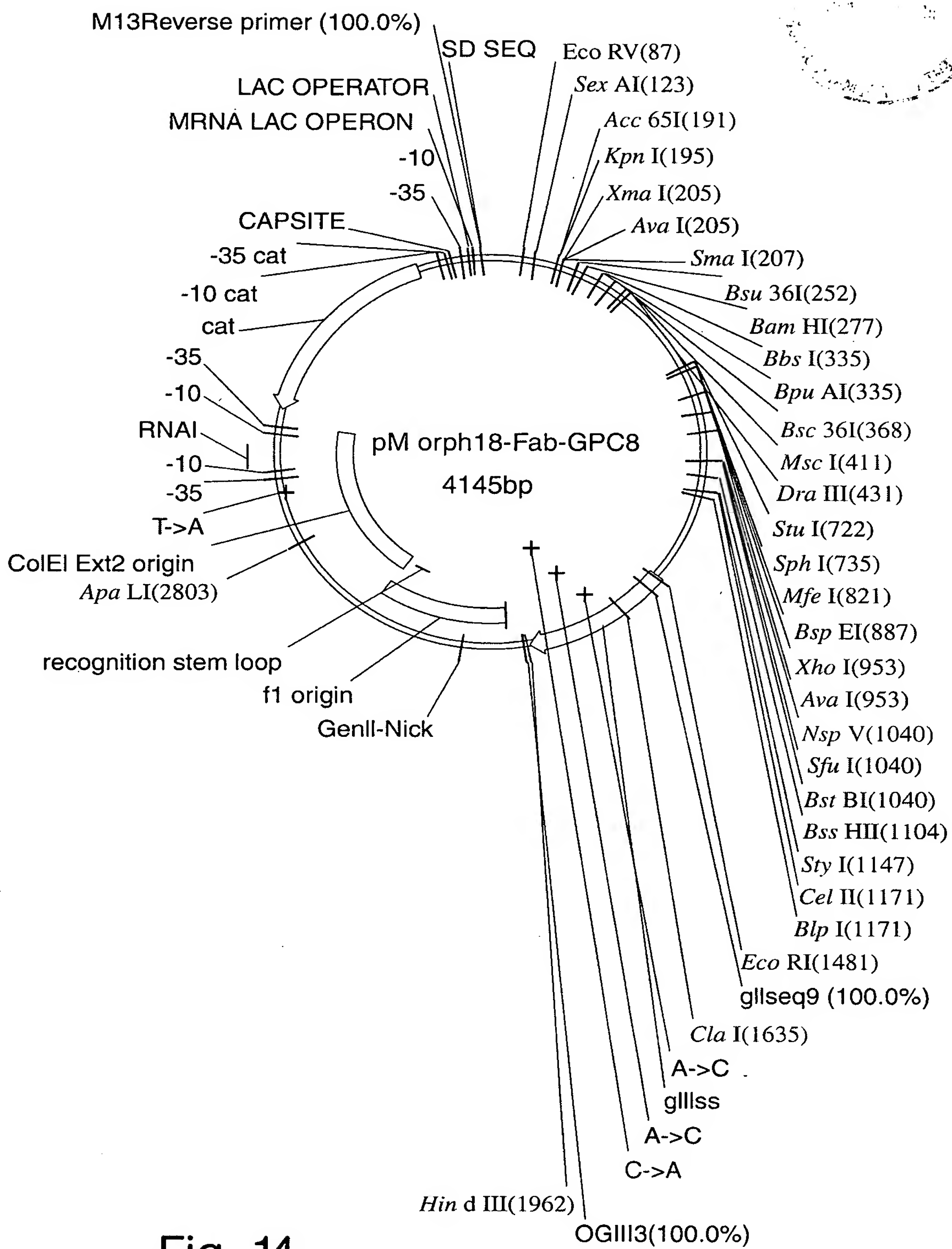


Fig. 14

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1 TCAGATAACG AGGGCAAAAA ATGAAAAAGA CAGCTATCGC GATTGCAGTG  
AGTCTATTGC TCCCGTTTTT TACTTTTTTCT GTCGATAGCG CTAACGTCAC

EcoRV  
~~~~~

51 GCACTGGCTG GTTTCGCTAC CGTAGCGCAG GCCGATATCG TGCTGACCCA  
CGTGACCGAC CAAAGCGATG GCATCGCGTC CGGCTATAGC ACGACTGGGT

SexAI  
~~~~~

101 GCCGCCTTCA GTGAGTGGCG CACCAGGTCA GCGTGTGACC ATCTCGTGTA  
CGGCGGAAGT CACTCACCGC GTGGTCCAGT CGCACACTGG TAGAGCACAT

KpnI  
~~~~~  
Acc65I  
~~~~~

151 GCGGCAGCAG CAGCAACATT GGCAGCAACT ATGTGAGCTG GTACCAGCAG  
CGCCGTCGTC GTCGTTGTAA CCGTCGTTGA TACACTCGAC CATGGTCGTC

XmaI  
~~~~~  
SmaI  
~~~~~  
AvaI  
~~~~~

Bsu36I  
~

201 TTGCCCCGGA CGGCGCCGAA ACTGCTGATT TATGATAACA ACCAGCGTCC  
AACGGGCCCT GCCGCGGCTT TGACGACTAA ATACTATTGT TGGTCGCAGG

Bsu36I  
~~~~~

BamHI  
~~~~~

251 CTCAGGCGTG CCGGATCGTT TTAGCGGATC CAAAGCGGC ACCAGCGCGA  
GAGTCCGCAC GGCTAGCAA AATCGCCTAG GTTTTCGCCG TGGTCGCGCT

BpuAI  
~~~~~  
BbsI  
~~~~~

301 GCCTTGCGAT TACGGGCCTG CAAAGCGAAG ACGAAGCGGA TTATTATTGC  
CGGAACGCTA ATGCCCGGAC GTTTCGCTTC TGCTTCGCCT AATAATAACG

Bsu36I  
~~~~~

351 CAGAGCTATG ACATGCCTCA GGCTGTGTTT GCGGCGGCA CGAAGTTTAA  
GTCTCGATAC TGTACGGAGT CCGACACAAA CCGCCGCCGT GCTTCAAATT

MscI  
~~~~~

DraIII  
~~~~~

401 CCGTTCTTGG CCAGCCGAAA GCCGCACCGA GTGTGACGCT GTTTCGCCCG  
GGCAAGAACC GGTCGGCTTT CGGCGTGGCT CACACTGCGA CAAAGGCGGC

451 AGCAGCGAAG AATTGCAGGC GAACAAAGCG ACCCTGGTGT GCCTGATTAG  
TCGTCGCTTC TTAACGTCCG CTTGTTTCGC TGGGACCACA CGGACTAATC

501 CGACTTTTAT CCGGGAGCCG TGACAGTGGC CTGGAAGGCA GATAGCAGCC

Fig. 14 (cont.)

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GCTGAAAATA GGCCCTCGGC ACTGTCACCG GACCTTCCGT CTATCGTCGG  
 551 CCGTCAAGGC GGGAGTGGAG ACCACCACAC CCTCCAAACA AAGCAACAAC  
 GGCAGTTCCG CCCTCACCTC TGGTGGTGTG GGAGGTTTGT TTCGTTGTTG  
 601 AAGTACGCGG CCAGCAGCTA TCTGAGCCTG ACGCCTGAGC AGTGGAAGTC  
 TTCATGCGCC GGTCGTCGAT AGACTCGGAC TCGGACTCG TCACCTTCAG  
 651 CCACAGAAGC TACAGCTGCC AGGTCACGCA TGAGGGGAGC ACCGTGGAAA  
 GGTGTCTTCG ATGTCGACGG TCCAGTGCGT ACTCCCCTCG TGGCACCTTT  
  
 StuI SphI  
 ~~~~~~  
 701 AAACCGTTGC GCCGACTGAG GCCTGATAAG CATGCGTAGG AGAAAATAAA  
 TTTGGCAACG CGGCTGACTC CGGACTATTC GTACGCATCC TCTTTTATTT  
 751 ATGAAACAAA GCACTATTGC ACTGGCACTC TTACCGTTGC TCTTCACCCC  
 TACTTTGTTT CGTGATAACG TGACCGTGAG AATGGCAACG AGAAGTGGGG  
  
 MfeI  
 ~~~~~~  
 801 TGTTACCAAA GCCCAGGTGC AATTGAAAGA AAGCGGCCCG GCCCTGGTGA  
 ACAATGGTTT CGGGTCCACG TTAAC TTTCT TTCGCCGGGC CGGGACCACT  
  
 BspEI  
 ~~~~~~  
 851 AACCGACCCA AACCTGACC CTGACCTGTA CCTTTTCCGG ATTTAGCCTG  
 TTGGCTGGGT TTGGGACTGG GACTGGACAT GGAAAAGGCC TAAATCGGAC  
 901 TCCACGTCTG GCGTTGGCGT GGGCTGGATT CGCCAGCCGC CTGGGAAAGC  
 AGGTGCAGAC CGCAACCGCA CCCGACCTAA GCGGTCGGCG GACCCTTTCTG  
  
 XhoI  
 ~~~~~~  
 AvaI  
 ~~~~~~  
 951 CCTCGAGTGG CTGGCTCTGA TTGATTGGGA TGATGATAAG TATTATAGCA  
 GGAGCTCACC GACCGAGACT AACTAACCCT ACTACTATTC ATAATATCGT  
  
 BstBI  
 ~~~~~~  
 SfuI  
 ~~~~~~  
 NspV  
 ~~~~~~  
 1001 CCAGCCTGAA AACGCGTCTG ACCATTAGCA AAGATACTTC GAAAAATCAG  
 GGTCGGACTT TTGCGCAGAC TGGTAATCGT TTCTATGAAG CTTTTTAGTC  
 1051 GTGGTGCTGA CTATGACCAA CATGGACCCG GTGGATACGG CCACCTATTA  
 CACCACGACT GATACTGGTT GTACCTGGGC CACCTATGCC GGTGGATAAT  
  
 BssHII StyI  
 ~~~~~~  
 1101 TTGCGCGCGT TCTCCTCGTT ATCGTGGTGC TTTTGATTAT TGGGGCCAAG  
 AACGCGCGCA AGAGGAGCAA TAGCACCACG AAAACTAATA ACCCCGGTTC

B1pI

Fig. 14 (cont.)



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StyI  
 ~~~~~  
 CelII  
 ~~~~~

1151	GCACCCTGGT	GACGGTTAGC	TCAGCGTCGA	CCAAAGGTCC	AAGCGTGTTT
	CGTGGGACCA	CTGCCAATCG	AGTCGCAGCT	GGTTTCCAGG	TTCGCACAAA
1201	CCGCTGGCTC	CGAGCAGCAA	AAGCACCAGC	GGCGGCACGG	CTGCCCTGGG
	GGCGACCGAG	GCTCGTCGTT	TTCGTGGTCG	CCGCCGTGCC	GACGGGACCC
1251	CTGCCTGGTT	AAAGATTATT	TCCCGGAACC	AGTCACCGTG	AGCTGGAACA
	GACGGACCAA	TTTCTAATAA	AGGGCCTTGG	TCAGTGGCAC	TCGACCTTGT
1301	GCGGGGCGCT	GACCAGCGGC	GTGCATACCT	TTCCGGCGGT	GCTGCAAAGC
	CGCCCCGCGA	CTGGTCGCCG	CACGTATGGA	AAGGCCGCCA	CGACGTTTCG
1351	AGCGGCCTGT	ATAGCCTGAG	CAGCGTTGTG	ACCGTGCCGA	GCAGCAGCTT
	TCGCCGGACA	TATCGGACTC	GTCGCAACAC	TGGCACGGCT	CGTCGTCGAA
1401	AGGCACTCAG	ACCTATATTT	GCAACGTGAA	CCATAAACCG	AGCAACACCA
	TCCGTGAGTC	TGGATATAAA	CGTTGCACTT	GGTATTTGGC	TCGTTGTGGT

EcoRI  
~~~~~

|      |            |            |            |            |            |
|------|------------|------------|------------|------------|------------|
| 1451 | AAGTGGATAA | AAAAGTGGAA | CCGAAAAGCG | AATTCGGGGG | AGGGAGCGGG |
|      | TTCACCTATT | TTTTACCTTT | GGCTTTTCGC | TTAAGCCCCC | TCCCTCGCCC |
| 1501 | AGCGGTGATT | TTGATTATGA | AAAGATGGCA | AACGCTAATA | AGGGGGCTAT |
|      | TCGCCACTAA | AACTAATACT | TTTCTACCGT | TTGCGATTAT | TCCCCCGATA |

gIIIseq9 100.0%  
=====

|      |            |            |            |            |            |
|------|------------|------------|------------|------------|------------|
| 1551 | GACCGAAAAT | GCCGATGAAA | ACGCGCTACA | GTCTGACGCT | AAAGGCAAAC |
|      | CTGGCTTTTA | CGGCTACTTT | TGCGCGATGT | CAGACTGCGA | TTTCCGTTTG |

ClaI  
~~~~~

1601	TTGATTCTGT	CGCTACTGAT	TACGGTGCTG	CTATCGATGG	TTTCATTGGT
	AACTAAGACA	GCGATGACTA	ATGCCACGAC	GATAGCTACC	AAAGTAACCA
1651	GACGTTTCCG	GCCTTGCTAA	TGGTAATGGT	GCTACTGGTG	ATTTTGCTGG
	CTGCAAAGGC	CGGAACGATT	ACCATTACCA	CGATGACCAC	TAAAACGACC
1701	CTCTAATTCC	CAAATGGCTC	AAGTCGGTGA	CGGTGATAAT	TCACCTTTAA
	GAGATTAAGG	GTTTACCGAG	TTCAGCCACT	GCCACTATTA	AGTGGA AATT
1751	TGAATAATTT	CCGTCAATAT	TTACCTTCCC	TCCCTCAATC	GGTTGAATGT
	ACTTATTAAA	GGCAGTTATA	AATGGAAGGG	AGGGAGTTAG	CCAAC TTACA
1801	CGCCCTTTTG	TCTTTGGCGC	TGGTAAACCA	TATGAATTTT	CTATTGATTG
	GCGGGAAAAC	AGAAACCGCG	ACCATTTGGT	ATACTTAAAA	GATAACTAAC
1851	TGACAAAATA	AACTTATTCC	GTGGTGTCTT	TGCGTTTCTT	TTATATGTTG
	ACTGTTTTAT	TTGAATAAGG	CACCACAGAA	ACGCAAAGAA	AATATACAAC
1901	CCACCTTTAT	GTATGTATTT	TCTACGTTTG	CTAACATACT	GCGTAATAAG
	GGTGGAATAA	CATACATAAA	AGATGCAAAC	GATTGTATGA	CGCATTATTC

Fig. 14 (cont.)

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## HindIII

~~~~~

1951 GAGTCTTGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG  
CTCAGAATA TTCGAAC TGG AACTTCACT TTTTACCGCG TCTAACACGC

OGIII3 100.0%

=====

2001 ACATTTTTTT TGTCTGCCGT TTAATGAAAT TGTAACGTT AATATTTTGT  
TGTAACAAAAC ACAGACGGCA AATTACTTTA ACATTTGCAA TTATAAAACA

2051 TAAAATTCGC GTTAAATTTT TGTTAAATCA GCTCATTTTT TAACCAATAG  
ATTTTAAGCG CAATTTAAAA ACAATTTAGT CGAGTAAAAA ATTGGTTATC

2101 GCGAAATCG GCAAAATCCC TTATAAATCA AAAGAATAGA CCGAGATAGG  
CGGCTTTAGC CGTTTTAGGG AATATTTAGT TTTCTTATCT GGCTCTATCC

2151 GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG  
CAACTCACAA CAAGGTCAAA CCTTGTTCTC AGGTGATAAT TTCTTGCACC

2201 ACTCCAACGT CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA  
TGAGGTTGCA GTTTCCTCGT TTTTGGCAGA TAGTCCCGCT ACCGGGTGAT

2251 CGAGAACCAT CACCCTAATC AAGTTTTTTG GGGTCGAGGT GCCGTAAAGC  
GCTCTTGGTA GTGGGATTAG TTCAAAAAC CCCAGCTCCA CGGCATTTCG

2301 ACTAAATCGG AACCTAAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA  
TGATTTAGCC TTGGGATTTT CCTCGGGGGC TAAATCTCGA ACTGCCCTT

2351 AGCCGGCGAA CGTGGCGAGA AAGGAAGGGA AGAAAGCGAA AGGAGCGGGC  
TCGGCCGCTT GCACCGCTCT TTCCTTCCCT TCTTTCGCTT TCCTCGCCCC

2401 GCTAGGGCGC TGGCAAGTGT AGCGGTCACG CTGCGCGTAA CCACCACACC  
CGATCCCGCG ACCGTTCA CA TCGCCAGTGC GACGCGCATT GGTGGTGTGG

2451 CGCCGCGCTT AATGCGCCGC TACAGGGCGC GTGCTAGCCA TGTGAGCAAA  
GCGGCGCGAA TTACGCGGCG ATGTCCCGCG CACGATCGGT ACACTCGTTT

2501 AGGCCAGCAA AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT  
TCCGGTCGTT TTCCGGTCCT TGGCATTTTT CCGGCGCAAC GACCGCAAAA

2551 TCCATAGGCT CCGCCCCCCT GACGAGCATC AAAAAAATCG ACGCTCAAGT  
AGGTATCCGA GCGGGGGGGA CTGCTCGTAG TGTTTTTAGC TGCAGATTCA

2601 CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC  
GTCTCCACCG CTTTGGGCTG TCCTGATATT TCTATGGTCC GCAAAGGGGG

2651 TGAAGCTCC CTCGTGCGCT CTCCTGTTCC GACCTGCCG CTTACCGGAT  
ACCTTCGAGG GAGCACGCGA GAGGACAAGG CTGGGACGGC GAATGGCCTA

2701 ACCTGTCCGC CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA  
TGGACAGGCG GAAAGAGGGA AGCCCTTCGC ACCGCGAAAG AGTATCGAGT

2751 CGCTGTAGGT ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG  
GCGACATCCA TAGAGTCAAG CCACATCCAG CAAGCGAGGT TCGACCCGAC

**ApaLI**

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Fig. 14 (cont.)

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2801	TGTGCACGAA ACACGTGCTT	CCCCCGTTC GGGGGGCAAG	AGTCCGACCG TCAGGCTGGC	CTGCGCCTTA GACGCGGAAT	TCCGGTAACT AGGCCATTGA
2851	ATCGTCTTGA TAGCAGAACT	GTCCAACCCG CAGGTTGGGC	GTAAGACACG CATTCTGTGC	ACTTATCGCC TGAATAGCGG	ACTGGCAGCA TGACCGTCGT
2901	GCCACTGGTA CGGTGACCAT	ACAGGATTAG TGTCTAATC	CAGAGCGAGG GTCTCGCTCC	TATGTAGGCG ATACATCCGC	GTGCTACAGA CACGATGTCT
2951	GTTCTTGAAG CAAGAACTTC	TGGTGGCCTA ACCACCGGAT	ACTACGGCTA TGATGCCGAT	CACTAGAAGA GTGATCTTCT	ACAGTATTTG TGTCATAAAC
3001	GTATCTGCGC CATAGACGCG	TCTGCTGTAG AGACGACATC	CCAGTTACCT GGTCAATGGA	TCGGAAAAAG AGCCTTTTTT	AGTTGGTAGC TCAACCATCG
3051	TCTTGATCCG AGAACTAGGC	GCAAACAAAC CGTTTGTTTG	CACCGCTGGT GTGGCGACCA	AGCGGTGGTT TCGCCACCAA	TTTTTGTTTG AAAAACAAAC
3101	CAAGCAGCAG GTTTCGTCGT	ATTACGCGCA TAATGCGCGT	GAAAAAAAGG CTTTTTTTTCC	ATCTCAAGAA TAGAGTTCTT	GATCCTTTGA CTAGGAAACT
3151	TCTTTTCTAC AGAAAAGATG	GGGGTCTGAC CCCCAGACTG	GCTCAGTGGA CGAGTCACCT	ACGAAAACCTC TGCTTTTGAG	ACGTTAAGGG TGCAATTCCC
3201	ATTTTGGTCA TAAAACCAGT	GATCTAGCAC CTAGATCGTG	CAGGCGTTTA GTCCGCAAAT	AGGGCACCAA TCCCGTGGTT	TAACTGCCTT ATTGACGGAA
3251	AAAAAAATTA TTTTTTTAAT	CGCCCCGCC GCGGGGCGGG	TGCCACTCAT ACGGTGAGTA	CGCAGTACTG GCGTCATGAC	TTGTAATTCA AACATTAAGT
3301	TTAAGCATT AATTCGTAAG	TGCCGACATG ACGGCTGTAC	GAAGCCATCA CTTCGGTAGT	CAAACGGCAT GTTTGCCGTA	GATGAACCTG CTACTTGGAC
3351	AATCGCCAGC TTAGCGGTCG	GGCATCAGCA CCGTAGTCGT	CCTTGTCGCC GGAACAGCGG	TTGCGTATAA AACGCATATT	TATTTGCCCA ATAAACGGGT
3401	TAGTGAAAAC ATCACTTTTG	GGGGGCGAAG CCCCCGCTTC	AAGTTGTCCA TTCAACAGGT	TATTGGCTAC ATAACCGATG	GTTTAAATCA CAAATTTAGT
3451	AAACTGGTGA TTTGACCACT	AACTCACCCA TTGAGTGGGT	GGGATTGGCT CCCTAACCGA	GAGACGAAAA CTCTGCTTTT	ACATATTCTC TGTATAAGAG
3501	AATAAACCTT TTATTTGGGA	TTAGGGAAAT AATCCCTTTA	AGGCCAGGTT TCCGGTCCAA	TTCACCGTAA AAGTGGCATT	CACGCCACAT GTGCGGTGTA
3551	CTTGCGAATA GAACGCTTAT	TATGTGTAGA ATACACATCT	AACTGCCGGA TTGACGGCCT	AATCGTCGTG TTAGCAGCAC	GTATTCCTC CATAAGTGAG
+1					
3601	CAGAGCGATG GTCTCGCTAC	AAAACGTTTC TTTTGCAAAG	AGTTTGCTCA TCAAACGAGT	TGGAAAACGG ACCTTTTGCC	TGTAACAAGG ACATTGTTCC
3651	GTGAACACTA CACTTGTGAT	TCCCATATCA AGGGTATAGT	CCAGCTCACC GGTCGAGTGG	GTCTTTCATT CAGAAAGTAA	GCCATACGGA CGGTATGCCT

Fig. 14 (cont.)



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3701	ACTCCGGGTG	AGCATTCATC	AGGCGGGCAA	GAATGTGAAT	AAAGGCCGGA
	TGAGGCCAC	TCGTAAGTAG	TCCGCCCGTT	CTTACACTTA	TTTCCGGCCT
3751	TAAAACTTGT	GCTTATTTTT	CTTTACGGTC	TTTAAAAAGG	CCGTAATATC
	ATTTTGAACA	CGAATAAAAA	GAAATGCCAG	AAATTTTTC	GGCATTATAG
3801	CAGCTGAACG	GTCTGGTTAT	AGGTACATTG	AGCAACTGAC	TGAAATGCCT
	GTCGACTTGC	CAGACCAATA	TCCATGTAAC	TCGTTGACTG	ACTTTACGGA
3851	CAAAATGTTC	TTTACGATGC	CATTGGGATA	TATCAACGGT	GGTATATCCA
	GTTTACAAAG	AAATGCTACG	GTAACCTTAT	ATAGTTGCCA	CCATATAGGT
3901	GTGATTTTTT	TCTCCATTTT	AGCTTCCTTA	GCTCCTGAAA	ATCTCGATAA
	CACTAAAAAA	AGAGGTAAAA	TCGAAGGAAT	CGAGGACTTT	TAGAGCTATT
3951	CTCAAAAAAT	ACGCCCCGTA	GTGATCTTAT	TTCAATTATG	TGAAAGTTGG
	GAGTTTTTTA	TGCGGGCCAT	CACTAGAATA	AAGTAATACC	ACTTTCAACC
4001	AACCTCACCC	GACGTCTAAT	GTGAGTTAGC	TCACTCATTA	GGCACCCAG
	TTGGAGTGGG	CTGCAGATTA	CACTCAATCG	AGTGAGTAAT	CCGTGGGGTC
4051	GCTTTACACT	TTATGCTTCC	GGCTCGTATG	TTGTGTGGAA	TTGTGAGCGG
	CGAAATGTGA	AATACGAAGG	CCGAGCATAC	AACACACCTT	AACACTCGCC
	M13 Reverse primer 100.0%				
	=====				
4101	ATAACAATTT	CACACAGGAA	ACAGCTATGA	CCATGATTAC	GAATT
	TATTGTTAAA	GTGTGTCCTT	TGTCGATACT	GGTACTAATG	CTTAA

Fig. 14 (cont.)